



ATPT2 : -----MES-----TSSSSSLVSAAGG-----FCWKKON-----LKLHSLSEIRVLRCDSSKVKVAKPK-----FR-----NNLVRP--DGQG : 59
ATPT3 : MAFFGLSRVSRRLKSSSVTPSSSSALLQSQHKSLSNPVTHYTNPTKCYPSWMDNYQVWSKGRELHOEKFVGWGNRYRLICGMSSSS : 90
ATPT4 : -----MWRRS--VYRFSRIISVSSSLPNRLIPWSREL-----CAVNSESPPTSTAKGICITGV-----RSD-----ANRVFA--TATA : 69
ATPT8 : -----MVLAEPKLAS-----AAEYFFKR-----GVQKQFR-----STILLMATA-----LN-----VRUPE--ALIG : 48
ATPT12 : -----MTS-----INNTVSTLHSSRVTSVDRVGVLSLRN-----SDSVEIRRR--SGFSLLIYESPCR-----REV-----VRAAE--DDDD : 64

ATPT2 : SSSLLLYP-----KHKSRFRVNAATAGQPEAFDSNSKQSFSDSADAFYRFSR-----PHTVIGTVLSILSVSFLAVEKVSIDISPLLTGILEA : 141
ATPT3 : SVLEGKEKKDDKEKSDGVVKKASWIDLYLPEEVRYAKLARDKPDTGTLWLAWECHWSIAL--AADPESLPSF--K-----YMALFGCG : 171
ATPT4 : AATATAT-----TG-EISSRVAALAGTGHYARCYWELSK-AKSMNLVATS-----GTGVLGT-GNAAISFPGL-----C--YTCA : 137
ATPT8 : ESTDIVT-----SELRVQRGIGMEITEMIHVASLLHDDVL-DDADTRRGVGS-----LNVVMGNKMSVLADGDFLLS-----RACG : 117
ATPT12 : KVKSQTE-----DKAPAGGSSINQLLGGK-ASQETNKWKIRLOITKPV-TWP-----PLVNGVCGAAASGNPHWTPED-----VAKSILQM : 140

ATPT2 : VVAALMMNIYIVGANOISDVIEDKVNKP--YLPLASGEYSVNTCHAIVASFSIMS-FMGVGVGSNPLFWA-----LFSFVLGTAM--SINL : 224
ATPT3 : AL-----LIRGAGCTINDLDDIDTKVDRKILPIASCLTPFOGTCGLQLLLG-LGILLQNNYS-----RVLGASSLLLVESY : 248
ATPT4 : GT--MMIAASANSINQIFESNDSKMKRTMLRPLPSGRISVPHAVAWATAGASCACILASKTNMLAAG-----LASANLVLYAFVATIP : 219
ATPT8 : AL--AALKNTEVVALLATAMEHLVTGET--MEITSTEQRYSDYVMQKTYKT--ASLHSNSCK-----AAVLTGQTAEVAV : 190
ATPT12 : MMSGPOLITGYTQTEINDWYDRDIDAINEP--YRPIPSGAMSEPEVITQVWLLGG-LGTAAGHDPVWAGHTTPTVLYALGGSLLS--YSA : 227

ATPT2 : PLRWKRFAALVAMCITAVRAITVQIAFVLIHQTHVFGRPILFTRPPIFATAFMSFFS-VVFAIFKIDIPDIEG-----KI : 299
ATPT3 : E-LMKRFTFWPOAFITGLT--INWGALLGHT--AVKGSHPASITIP--LYLSGVCWTLVYDTIYAHQDKED-----D-----VK : 314
ATPT4 : LKQLHPINTWCAVW-----GAPPLLGWA-----AASQITSYNSMILPAALYFWQTPHFAHLCRNDYAAAGGYKMLSLFDPGKRIAA : 300
ATPT8 : LAFEYGRNLGLAFQII-----DDIDDFGTIS-----ASLKGSLSDIRHGVIIPILFAMEEPQIREVVDQVEK-----DP-----RN : 259
ATPT12 : EPEKLRQNGWGNFA-LG--ASYNISLPPWAGQ--ALFGTLTPDVVVL-----LLYSIAG-LGTAANDFKSNEG-----D-----SA : 294

ATPT2 : FGIRG-----FSVTLGQ-----KRVFMTC--VTELOMAYVAVAILVCAITSPFPWSK-----VISVGHVILATTLWARAKSVLSSKTEITSCY : 375
ATPT3 : GGVKS-----TAPREGD-----NKKLITGTGTHASIGFLAUSGFSADLGWQYVAS-----LAASGQLGQIGTADLSSGADCSRKFVSNKWE : 392
ATPT4 : VALRNCFYMIPICHIAYDWGLISSMFGLESLTLTAIATATASFYDRDTHKARKMFHASEFLPVMGSLLLHRVSNNDNQOOLVEEAGL : 390
ATPT8 : VDIAL-----EVLGKSK-----GLO--RAREMEHNLALMAIGSPET-----DNEVKKRRRALIDLTHRVITRNK----- : 321
ATPT12 : LGLQS-----LPVAFGT-----EPAKMIG-VGADITQLSVAGMLLSGKPYMALA--LVALLTPQLVQFKYFLKDPVKYDVKYQASAOQPE : 373

ATPT2 : MFIWKL FYAE-----YLLLPFLK----- : 393
ATPT3 : GAIIFSGVVLG-----RSFO----- : 407
ATPT4 : TNSVSGEVKTQRKRKRVAPPPVAYASAAPPPFLPAPSFYSP : 431
ATPT8 : ----- : -
ATPT12 : --LVLGIFVTA-----LASOH----- : 387

Figure 1

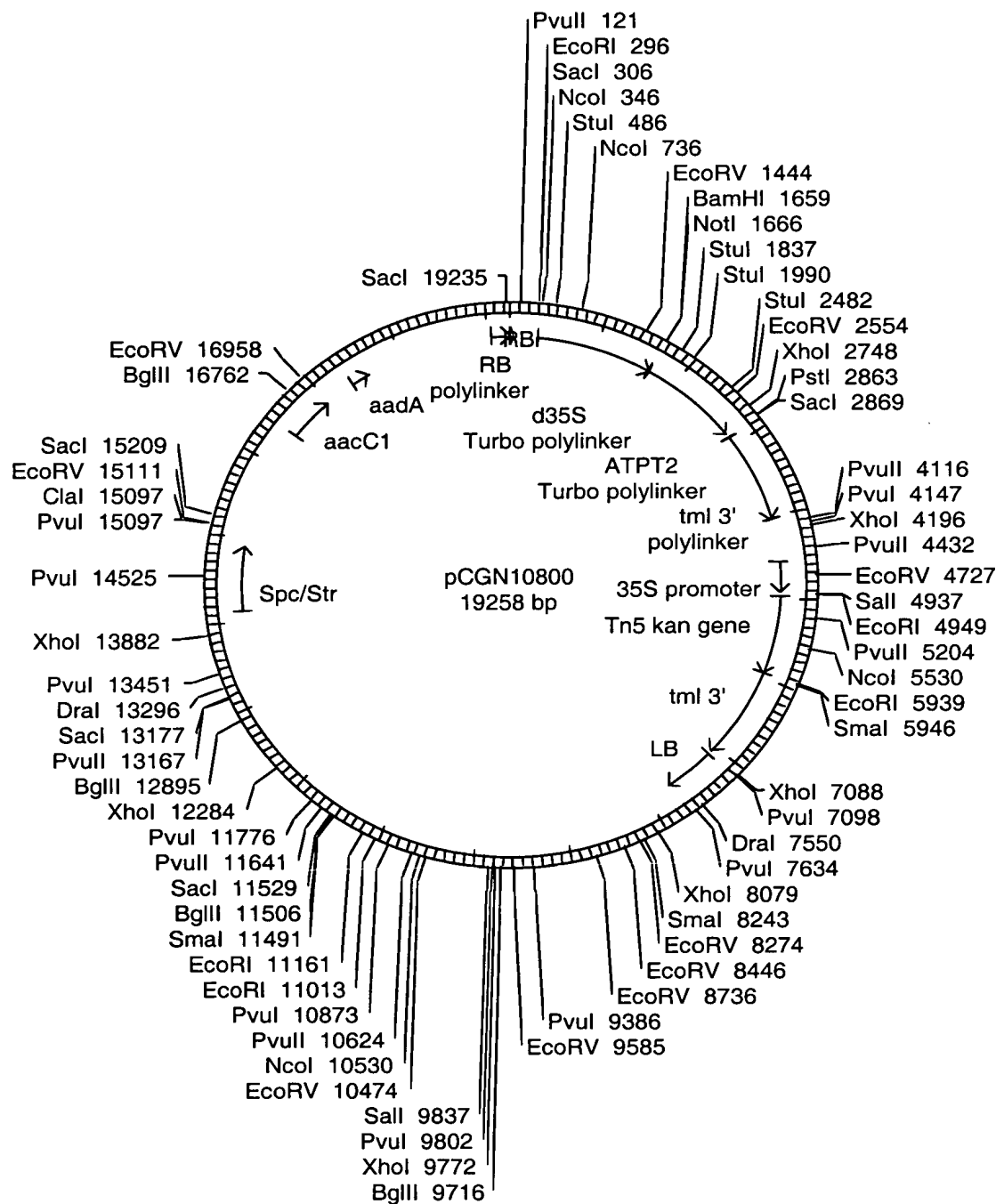


Figure 2

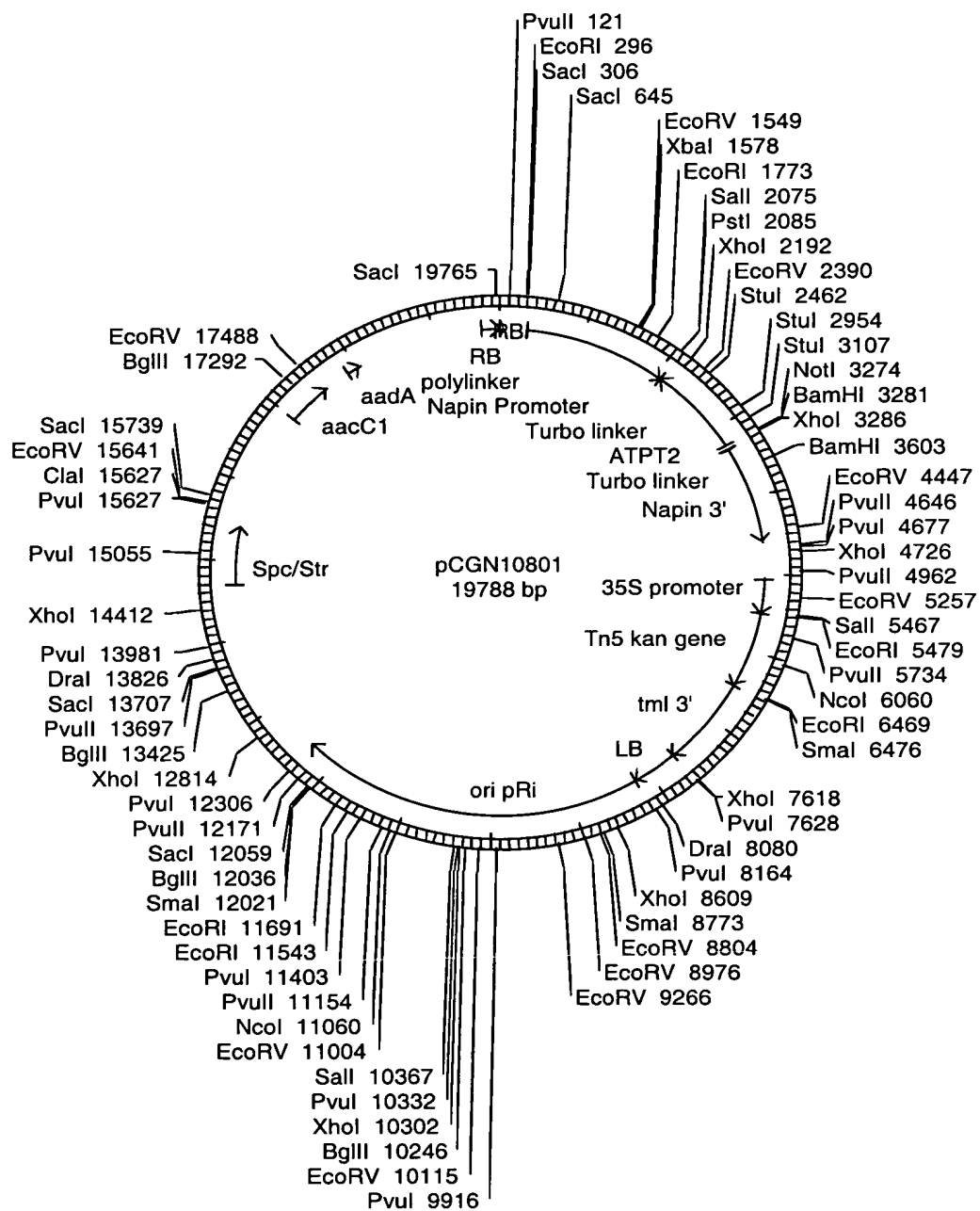


Figure 3

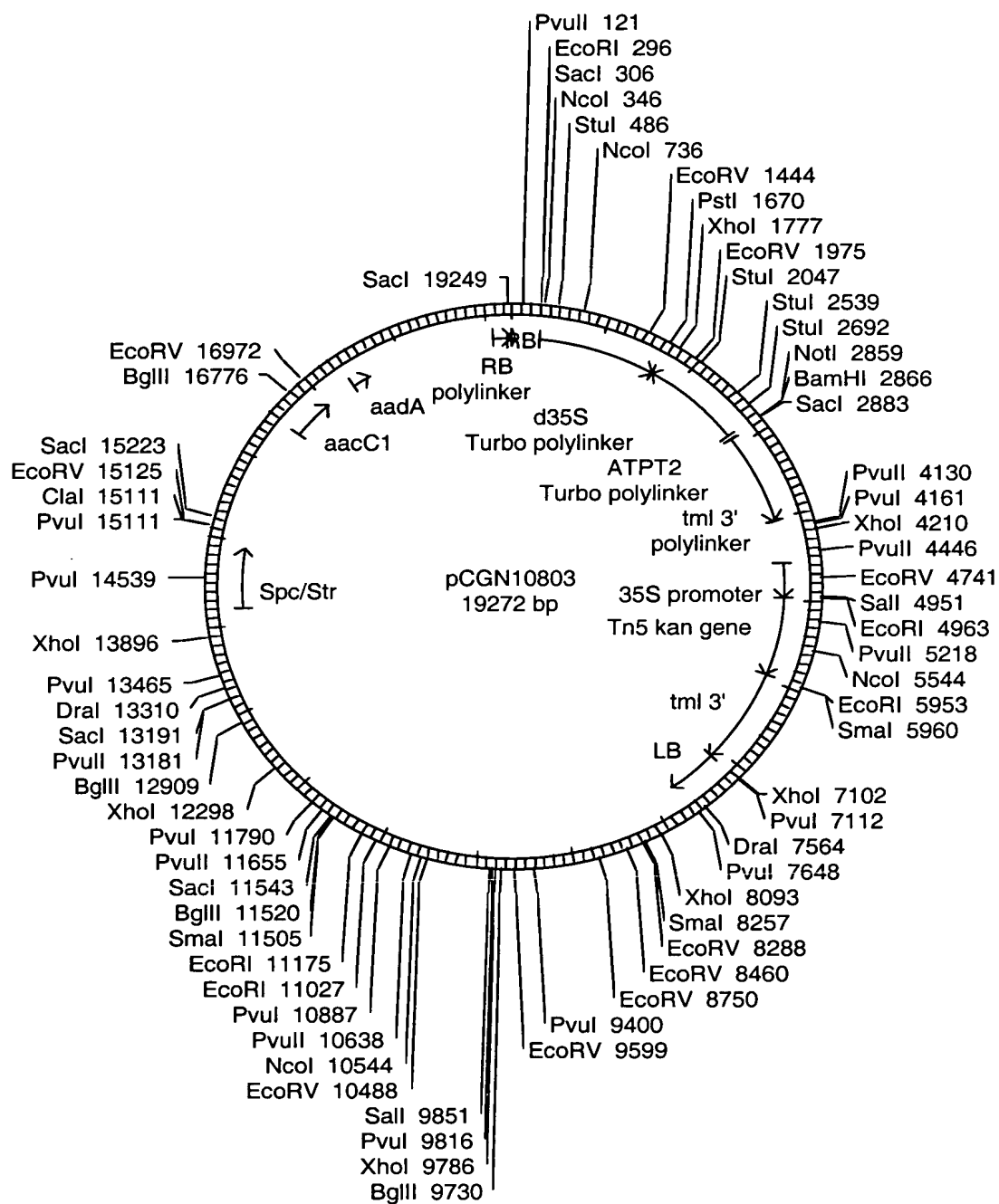


Figure 4

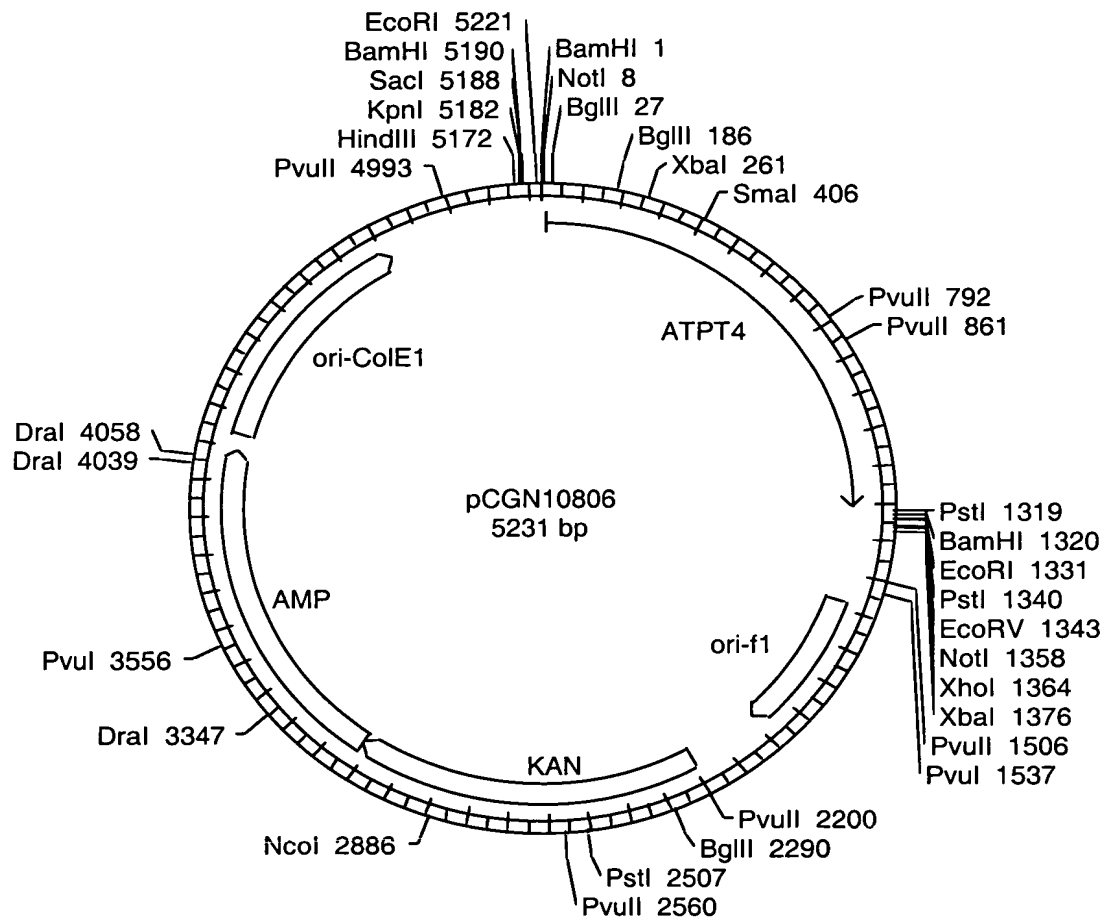


Figure 5

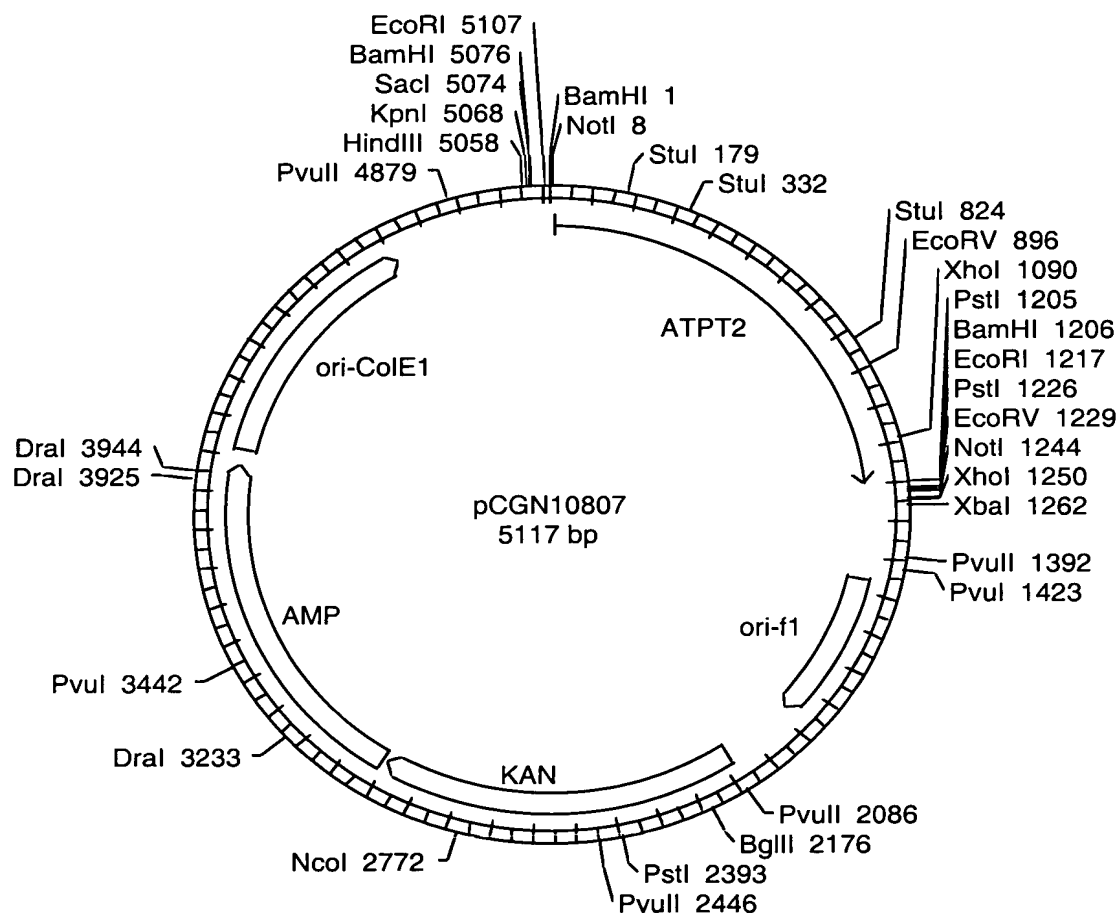


Figure 6

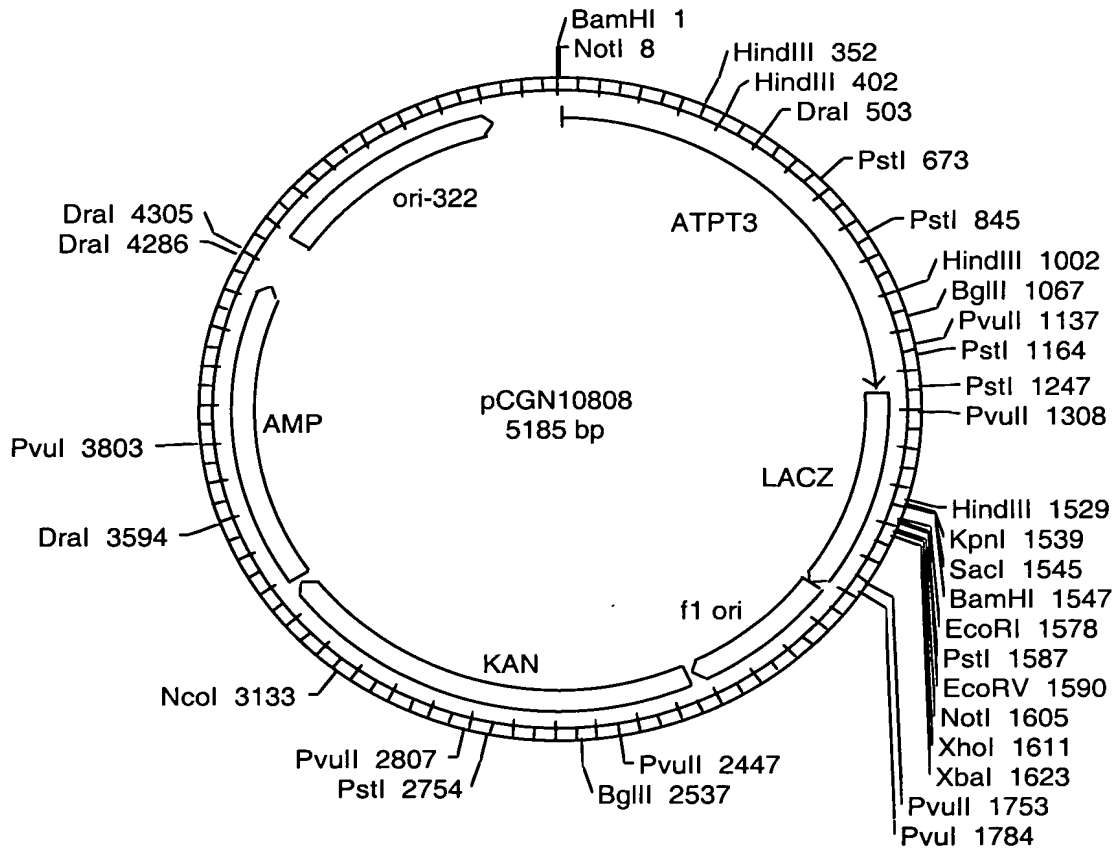


Figure 7

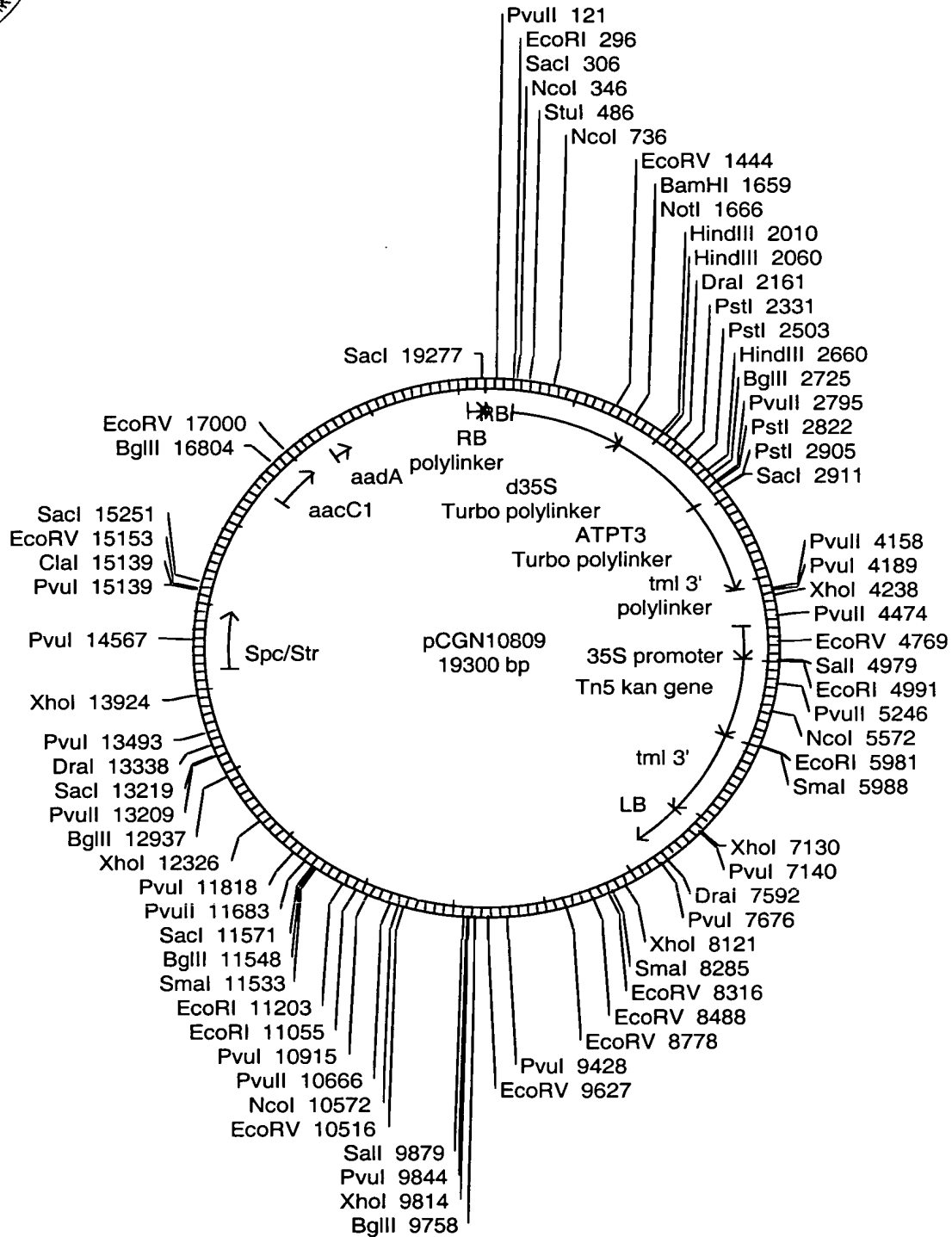


Figure 8

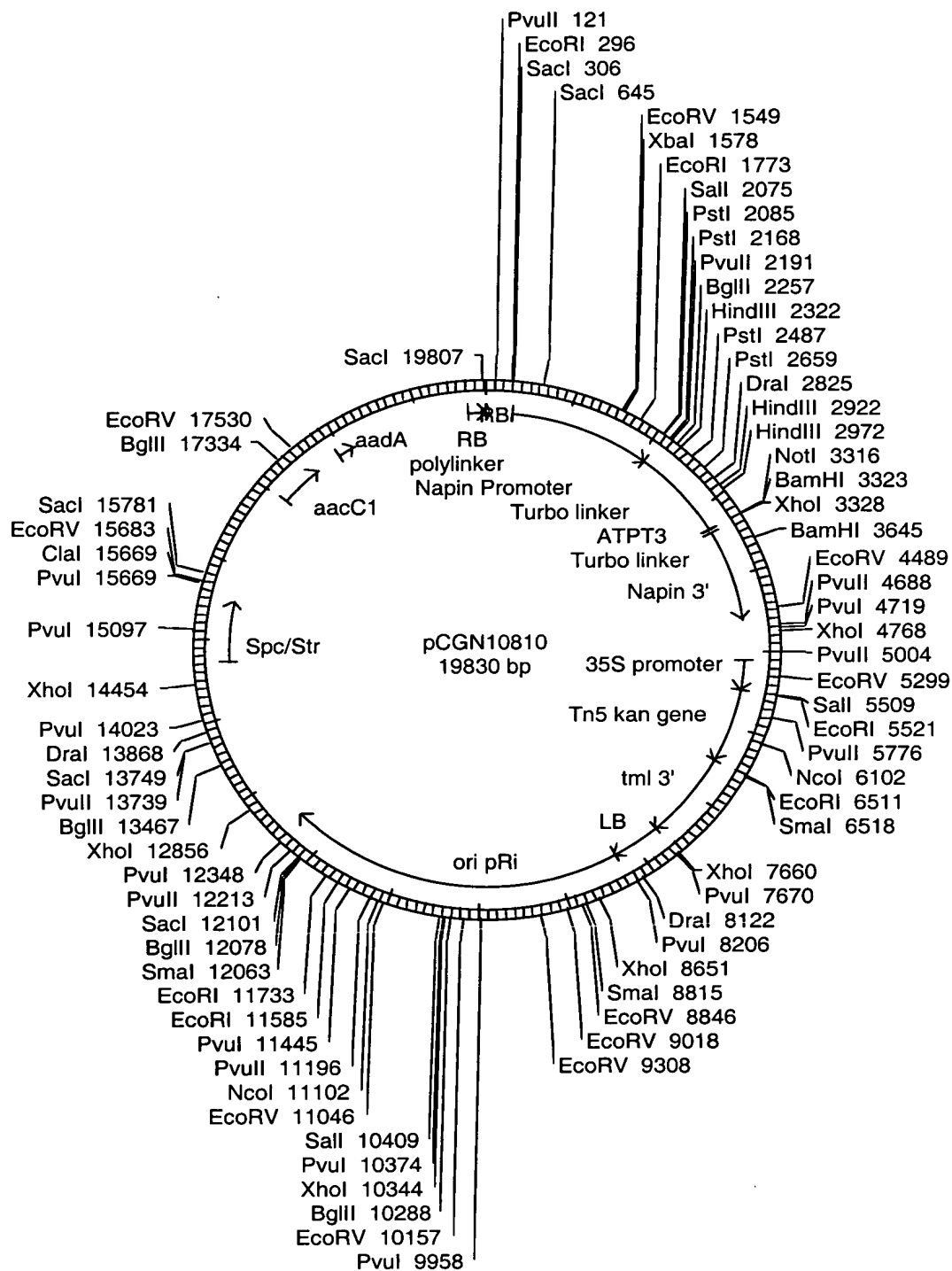


Figure 9

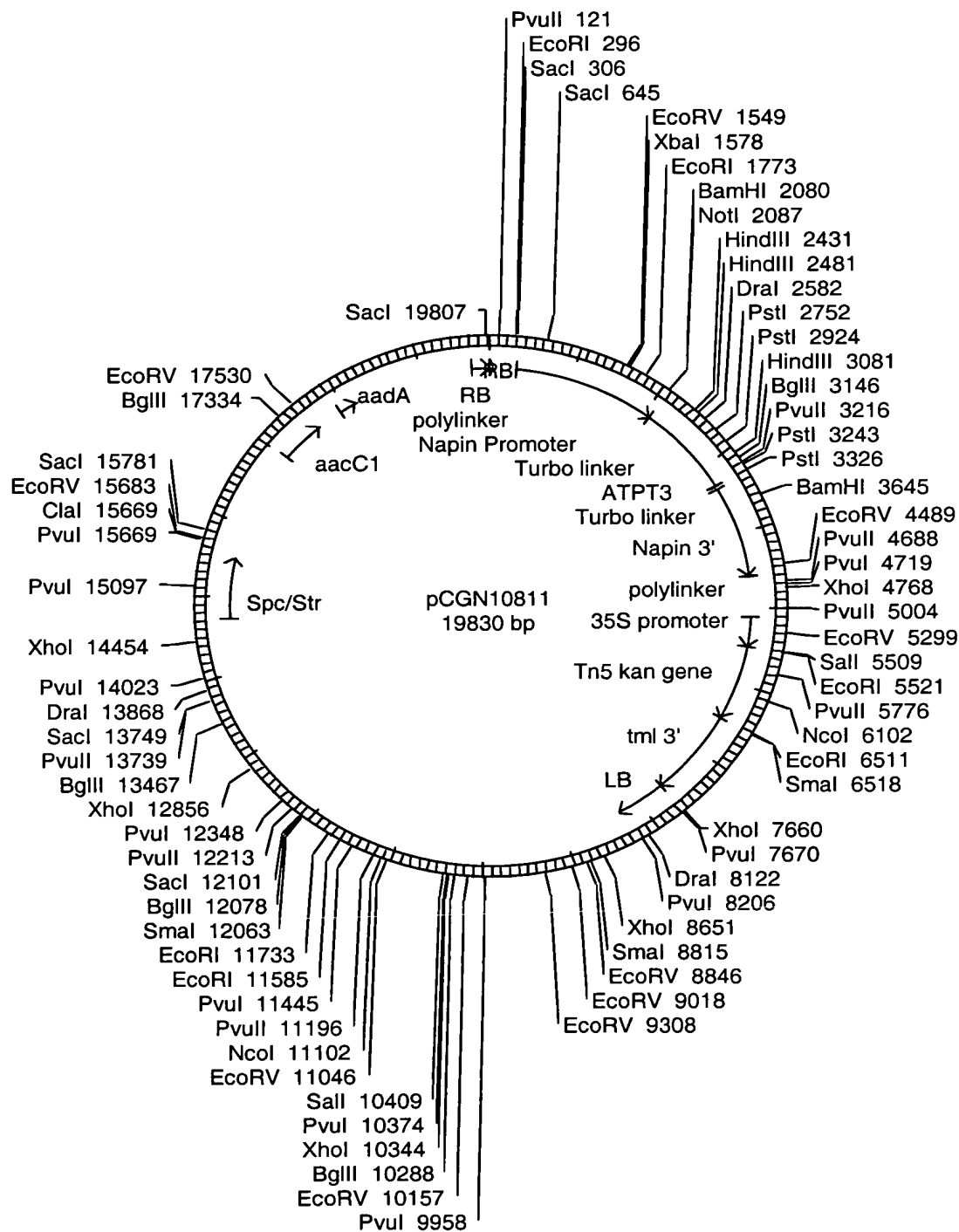


Figure 10

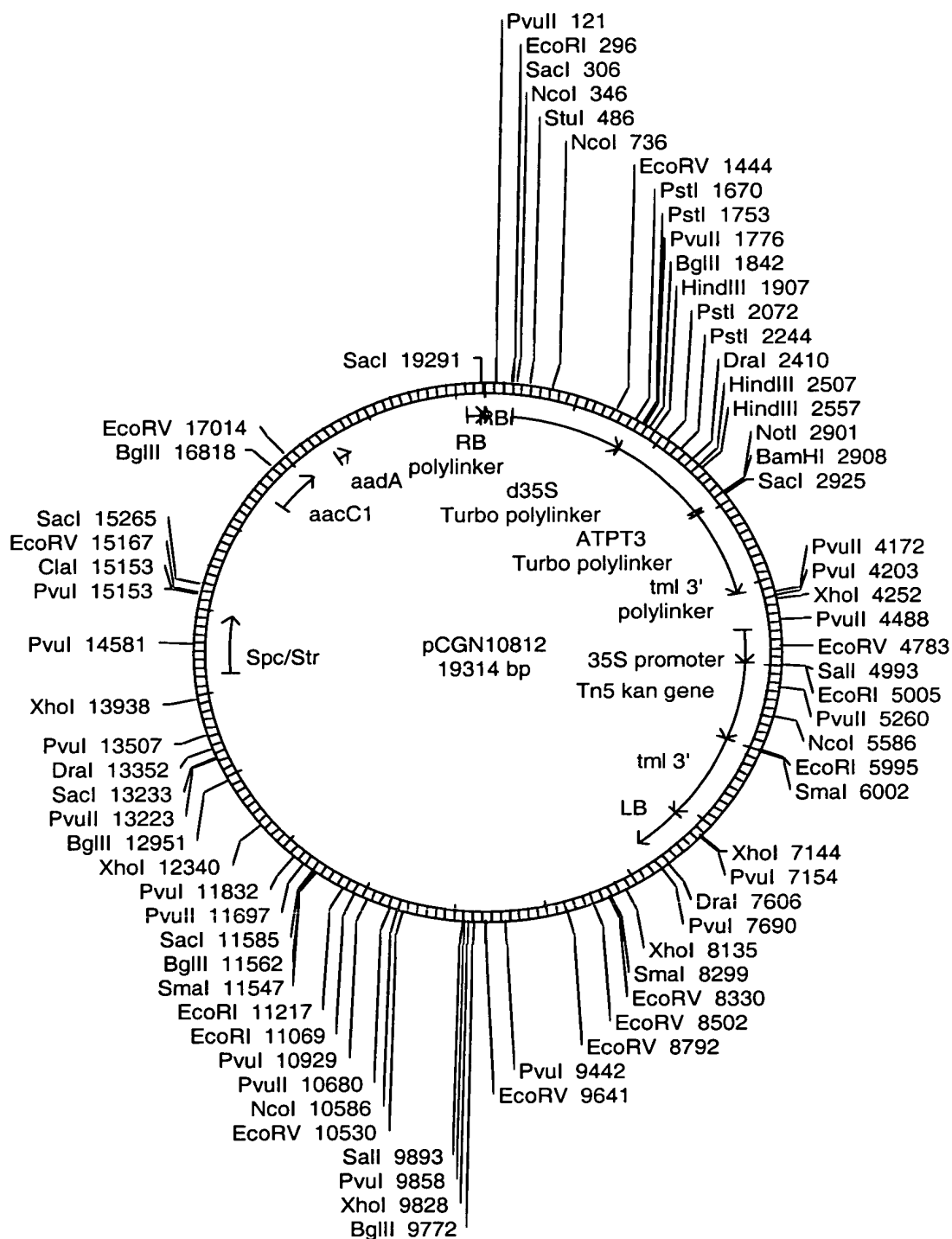


Figure 11

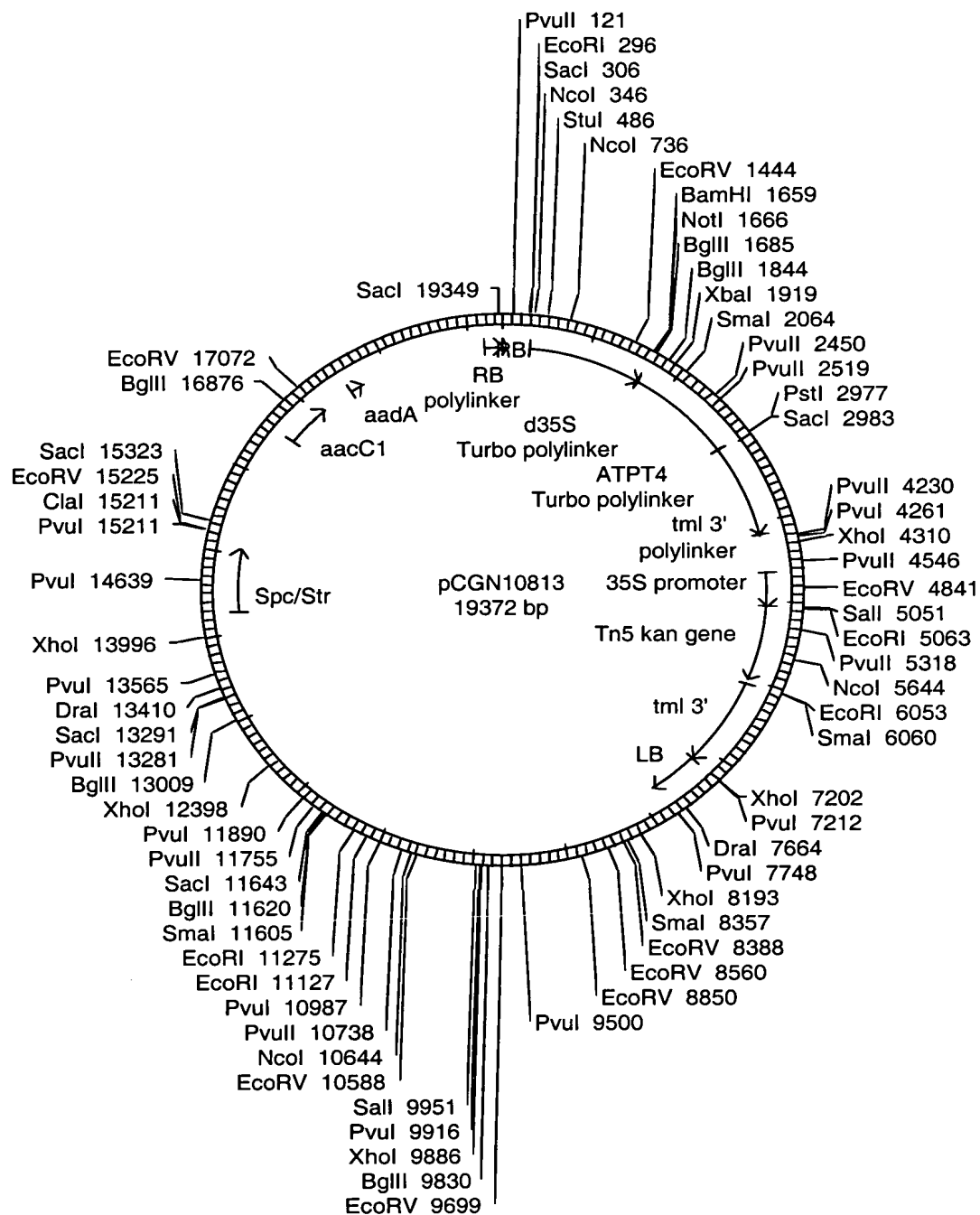


Figure 12

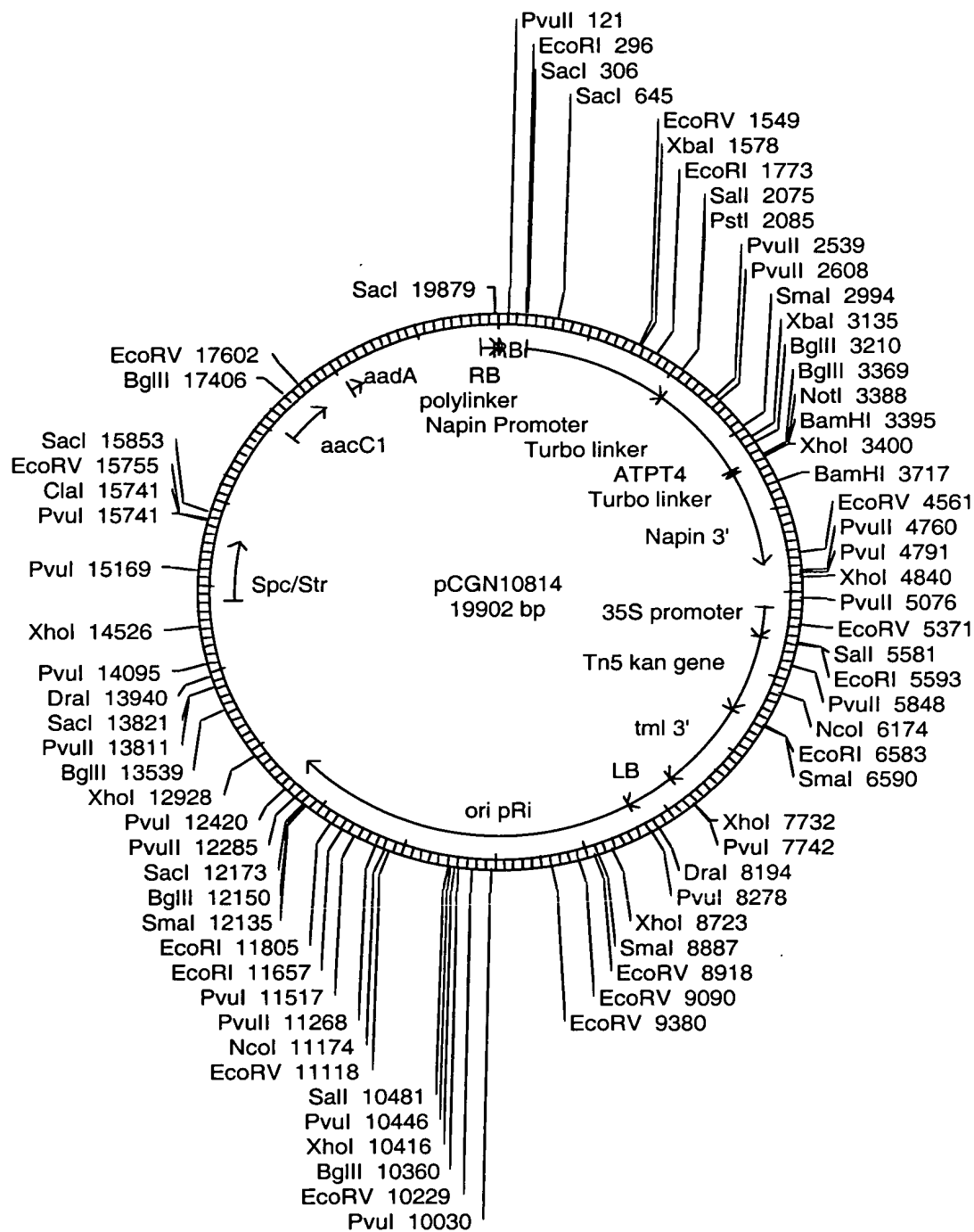


Figure 13

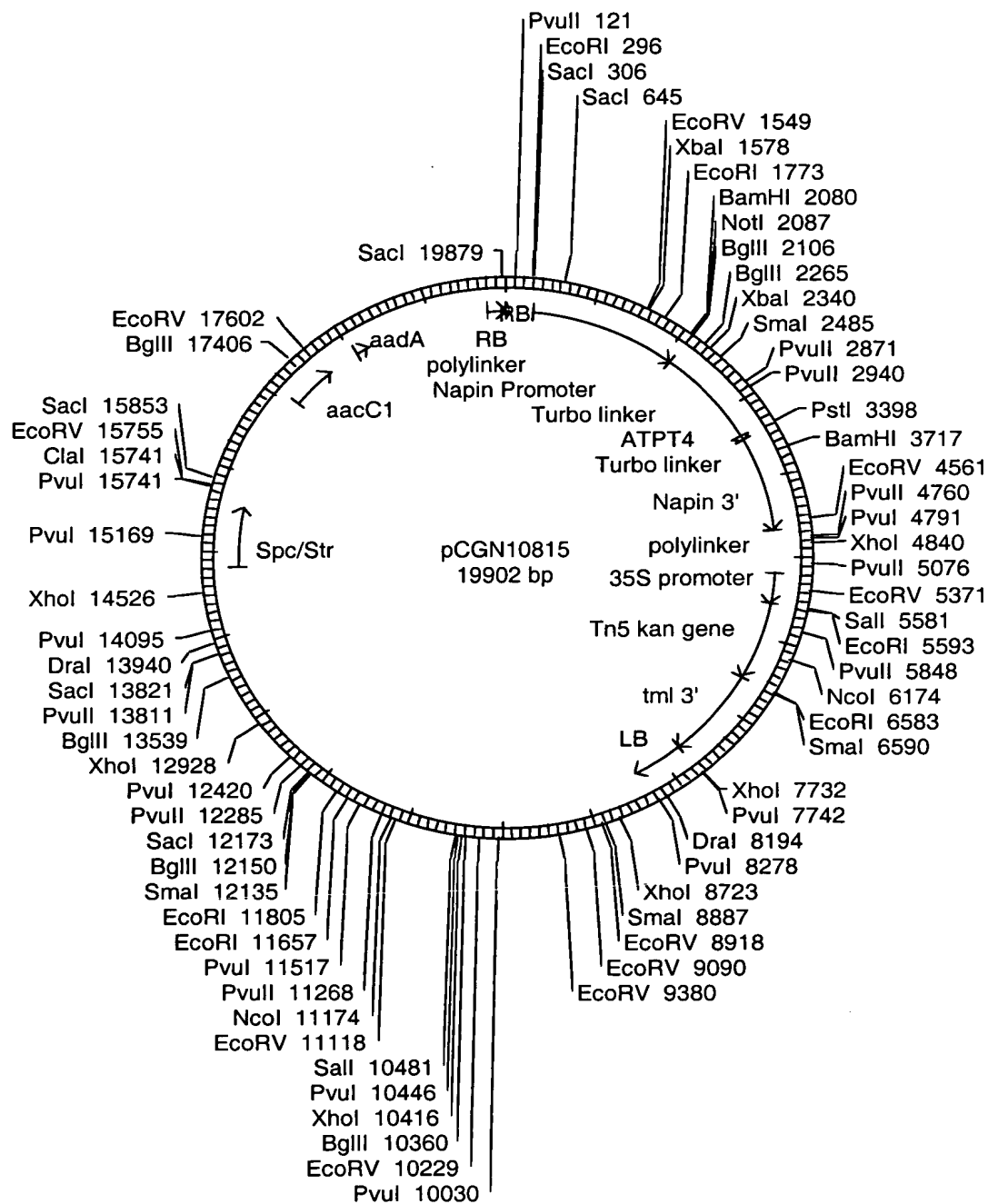


Figure 14

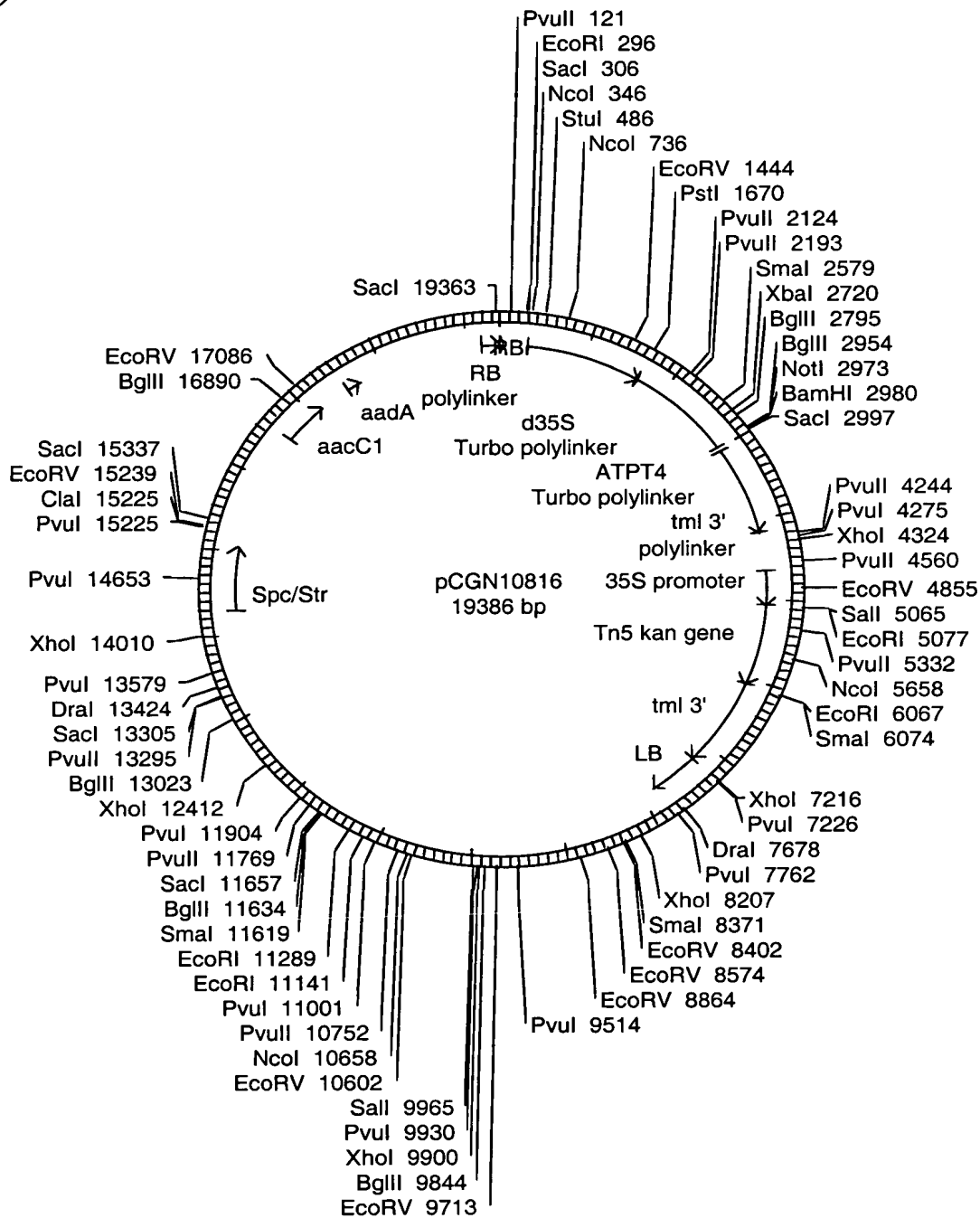


Figure 15

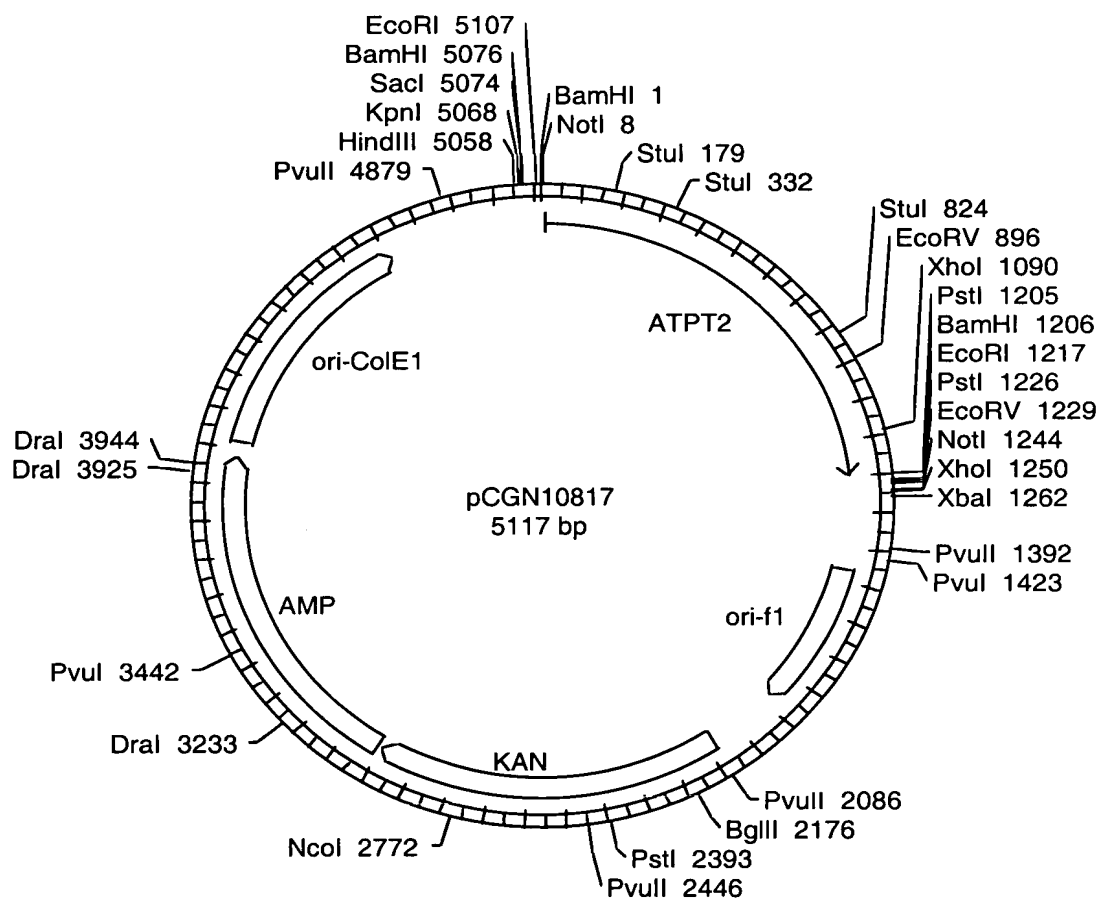


Figure 16

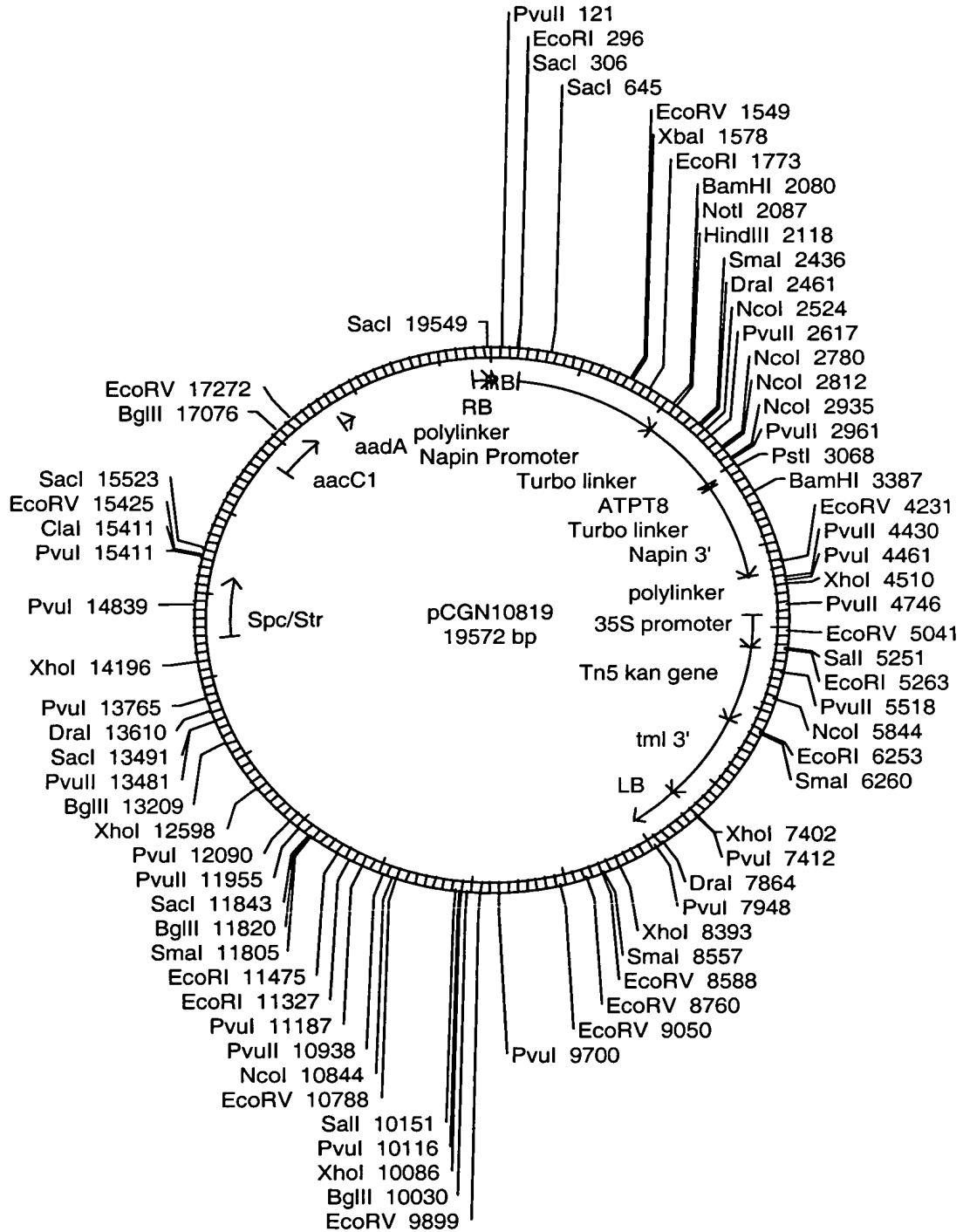


Figure 17

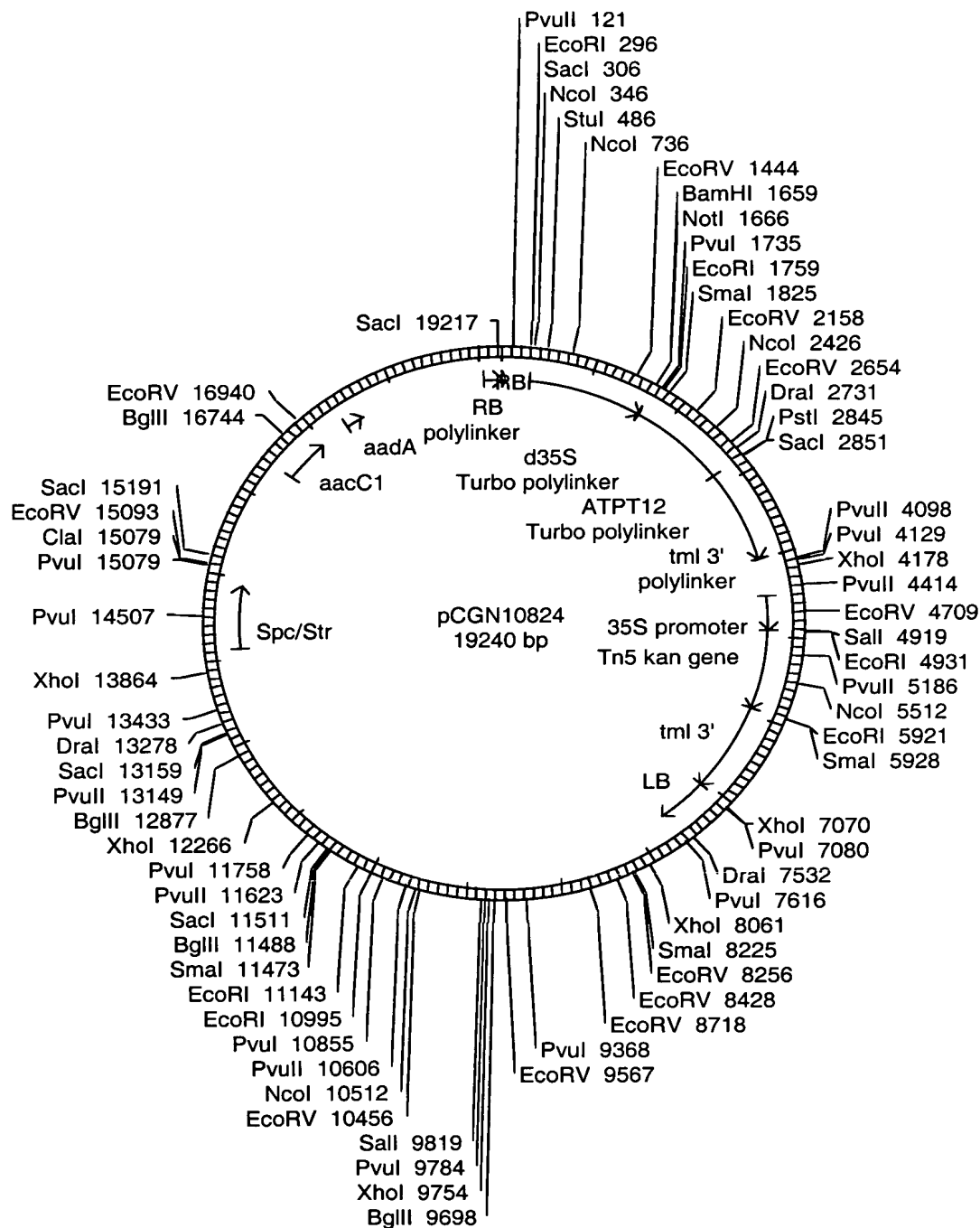
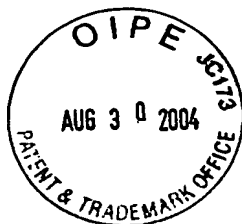


Figure 18

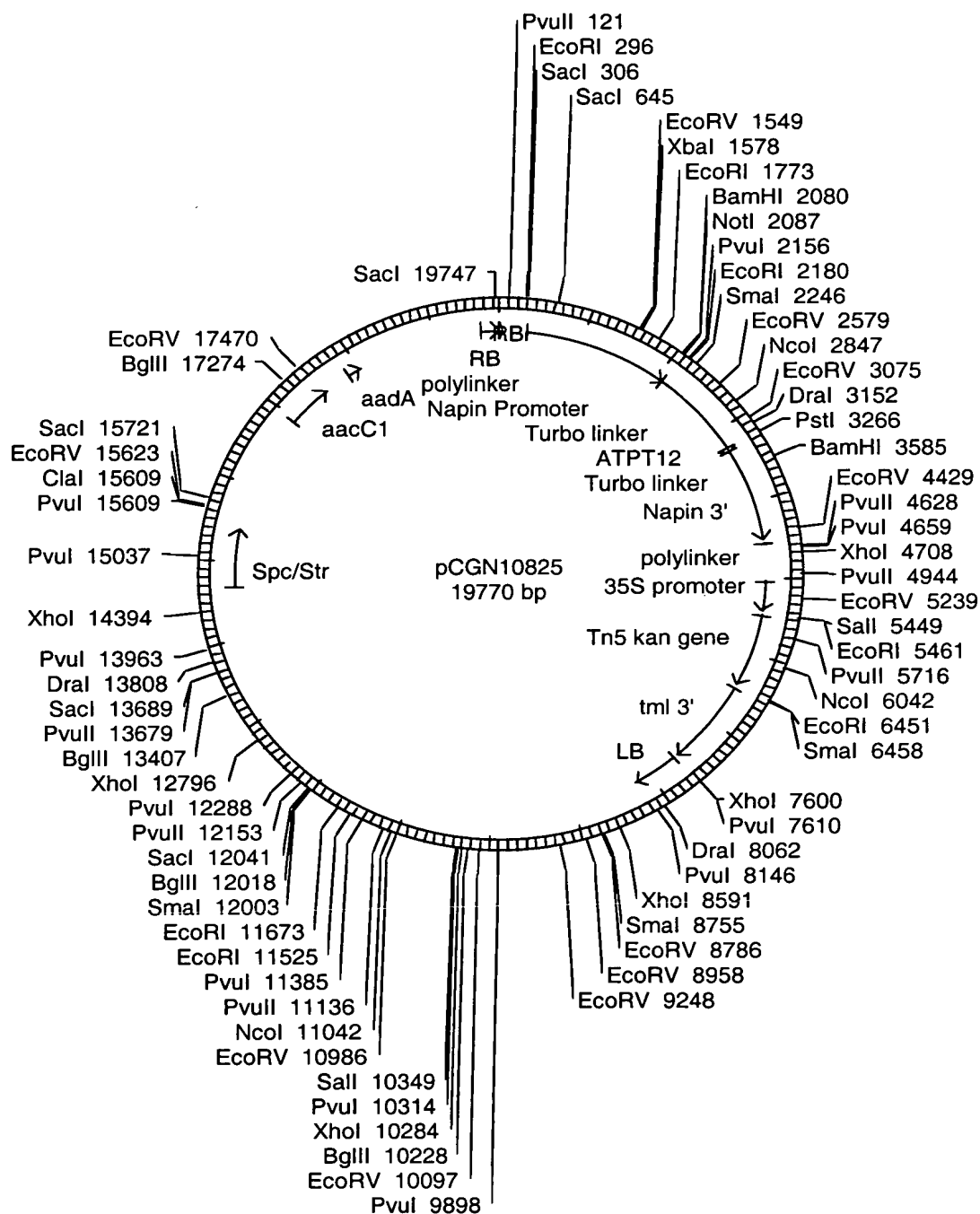


Figure 19

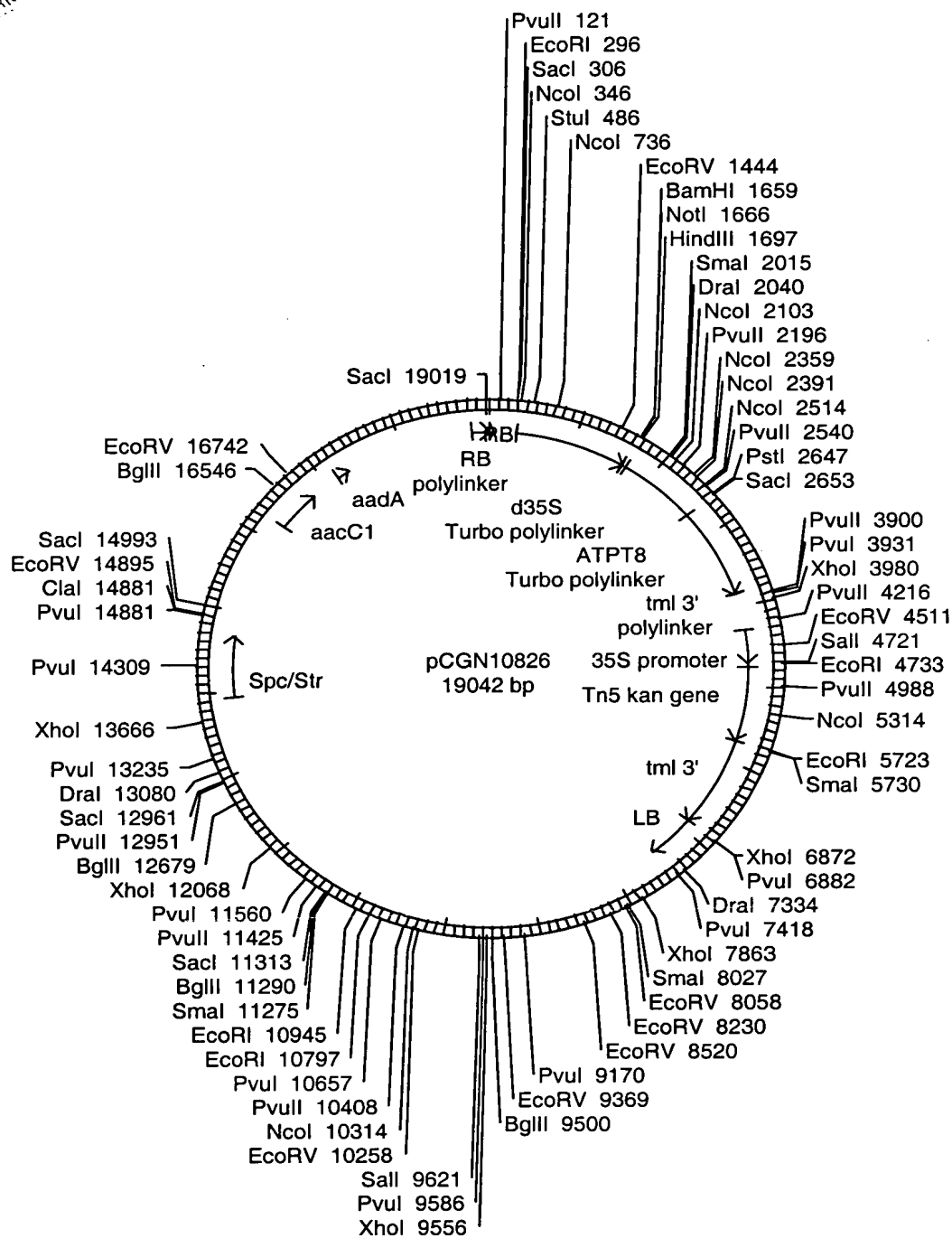


Figure 20

SLR1736 : MATIQAFWR-----FSRPHTIIIGTTLS-----VWAVYLLITLGLD--G-NSVNSPAS-----IDLIVFGAWBACELGNNVIVIGL : 64
 SLR0926 : MVAQTPSS---PPLWLTIILYLRWHKP-----AGRLIIMIDALWA--VCLAAQGLPP-----LPIHGTIACGTATSGLCGVV : 68
 SL11899 : MVTSTKIHRQDSMCVCKSYQLTTP-----RIPIILLITTAAS--MWIASEGRVD-----LPKLLITLGGTAAASAQTL : 71
 SLR0056 : MSDIIONTQ--NOAKAPQLLGMKGAAPGESIWKIRLOMKPITWIPILWGVVCCAASSGGYIWSVEDFKALATCMILSGPIMTGVTQTL : 88
 SLR1518 : MTESSPLAP--STAPATRKLMIAAIKP-----PMYTVAVVPIITVGSAAVAYGLITCQWH-----GDVFTTIFLSAIAIAINLS : 71
 M : 1 L
 SLR1736 : NQLMVDIEDRINKPNLPLANGDFSIAQGRWIVGTCGVASIAIAWGLMGLGLTVGIS--LITGTAVSVPPVRLKRFSLLAALCITITVRGH : 152
 SLR0926 : NDLMDRDIDPOVERTKORPLAARAL--SVQVCGIGVALVA--LLCAAGAFYITPLS-----FMLCVAAAPVIVAYPGAKRVFPVQVLVLSH : 150
 SL11899 : NCTYDQDHDYEMLTRARPPIPAKGV--OPRHAIIFALALGVLSFALHAFWNLVSGC---LPAUSGIVFYMLVYTHWLKRHTAQNIIVIGGA : 156
 SLR0056 : NDFYDRDIIDAINERYEPTESGAI SVPOVVTQILLLLVAGIGVAYGCDVWQAQHDFFPIMMVITLGGAFVAYIYSAPPLKQKQWGLGNY-AL : 177
 SLR1518 : NDVFDSDTIGIDVFRKAHSVWNLTGNRNILFLISNFFLLAGVILGLMSWSWRAQDWI-----VLELIGVAIIFGYTYQGPFRFLGYLGLGELIC : 157
 N : 5D Did 1 a 6 6 1 6
 SLR1736 : VVNGLFLIFRIGLCYPPPIITPWNVLFHFLVFTVAIAIFKVDVPMVEGDROPKIQTITLQIKQNVFRGTLITLTG-CYLAIAIWGLWA : 241
 SLR0926 : AWGFAVLISWS---AVTGDIDATVNLWGATVFWLIGDFTVYAMADREDDRIGVNSSALPFG-CYVGEAVGUFFA--LITIGCLFYITGMI : 234
 SL11899 : AGSIPPLVGMMA---AVTGDLSWTPWNLFAFLFWPPHFWALAMIKDDYAQNVVPMIPVIAAGEKTVSQIWIYSD--LVVPFSLLYYP : 241
 SLR0056 : GASVIALPWAG-HALFCTENPTWMLIYSLAGIGAVNDFKSVGEDROLGKSPWVFG-IGTAAWICVYMW--DVFOAGIAGYLI : 263
 SLR1518 : LIIEGLPLAIAAAVYSQSQSFVSNLLTSPVTVGISTAILFCSHFHQVEDDLAAGKKSPIVRLC-TKIGSQVLTISVSYIITAGVICH : 246
 1 l v1 t e d 6 G
 SLR1736 : 280 * 300 * 320 * 340
 SLR0926 : AMPLNTAFITVSHDCTIALLLWRSRDVHLESKTEIASFYQFIWKIEHFFLEVILLYPLALWLPNFSNTIF----- : 308
 SLR1518 : LMLNPLYWLSHAFATVGVVIOYIQLSAPTEEPKLYGQ--IEGQNVLIGFVLLAGMLLGMW----- : 292
 SL11899 : LHQLGLIYLAIAHIGGQFLVKAWQLKQAPGDRDLTARG-LEKFSFHYLMILCLAMVIDSLPVTHQLVAQMGTLLG : 316
 SLR0056 : YWQQEYATIVLLETPONTFQDMYFLRNPLENDVKYQ-ASAQPTLVFGMLATGALGHAGI----- : 324
 SLR1518 : QAPWQTLTLLIASLPWAVQLIRHVQYXHDQEQVSNCKFIAVNLHFFSGMLMAAGYWGAGG----- : 307
 p 6

Figure 21

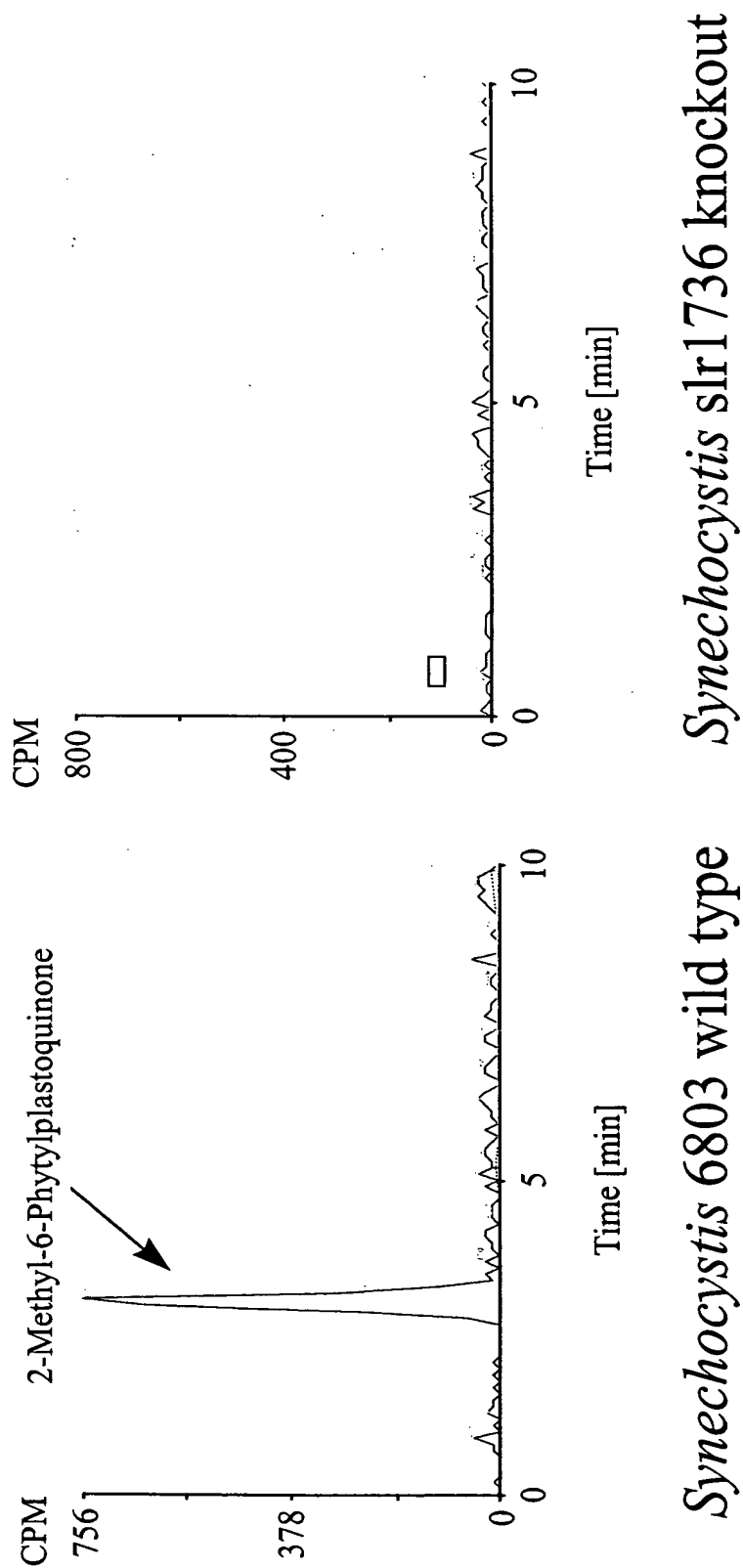


	*	20	*	40	*	60	*	80						
ATPT2	:	----	--	MESLSSSLVSAAGGFCWKKQNLKLHSLSEIRVLRCDSSKVVAKPKFRNNLVRPDGQSSLLLYPKHKSFRVNATAGQ	:	80								
SLR1736	:	----	----	-----	----	-----	----	-----	----					
ATPT3	:	MAFFGLSRVSRLLKSSSVTPSPSSSALLQSQHKSLSNPVTHYTNPTFTKCYPSWNDNYQVWSKGRLEHOKEFFGVGWNYRLICGMSSS	:	89										
SLR0926	:	----	----	-----	----	-----	----	-----	----					
ATPT4	:	-----	-----	MWRRSVVYRFSSRISVSSSLPNRPLIPWSRELCAVNSFSQP	:	67								
SLL1899	:	----	----	-----	----	-----	----	-----	----					
ATPT12	:	-----	-----	MTSILNTVSTIHSRVTSDRVGVLSLRNSDSVEFT	:	4								
SLR0056	:	-----	-----	-----	-----	-----	-----	-----	-----					
ATPT8	:	-----	-----	-----	-----	-----	-----	-----	-----					
SLR1518	:	-----	-----	-----	-----	-----	-----	-----	-----					
	*	100	*	120	*	140	*	160	*					
ATPT2	:	PEAFDSNSKQK	----	SFRDSDDAFYR	----	FSRPHTVIGTVLSHLS	----	VSLAVEKVS	----	DISPLEFTGLE	:	140		
SLR1736	:	-----	-----	MATHQAFWR	----	FSRPHTVIGTVLSWAVY	----	LLTILGDGN	----	SVNSPASDLMVFG	:	49		
ATPT3	:	SSVLEGPKKDDKEKSDGVVVKASWIDLYLPEEVGRYAKLARLDKPIGTWLLAWPCWMS	:	170				IALAADPGS	----	LPSFKYNALFGC	:	170		
SLR0926	:	-----	-----	PLWHTIYYL	----	LRWHKPAGRLHLMIPALWA	----	VCIAAQ	----	G	----	LPPLPELGLTAL	:	56
ATPT4	:	TAAATATATTG	----	EISSRVAALAGLGHYAR	----	CYWELSKAKLSMLVVATSG	----	TGVILGTGNAAISFPGHCYTCAG	:	138				
SLL1899	:	TKIHRQDSMG	----	AVCKSYQLTKP	----	RIPLLLHTTAASMMI	----	ASEGR	----	VDLPKEHITILG	:	60		
ATPT12	:	DKVKSQTPDKAP	----	AGSSINQLLGKAS	----	QETNKWKIRQLTKPVTMPPLVGVVCCGAASGNFHWTPEDVAKSILC	:	139						
SLR0056	:	QNT	----	GQNOAKA	----	RQLGKKAAP	----	GESSIWKIRQLMKPITMPLIWGVVCCGAASSGGYIWSVEDFKALUTC	:	73				
ATPT8	:	EVPKLASAAEY	----	FFKRGVQKQF	----	RSTILLATATALNVRVP	----	EALIGEST	----	DIVTSELRVRQR	:	63		
SLR1518	:	SPLAPSTAPAT	----	RKLWAAIKP	----	PMYTVAVVPITVG	----	SAVAYGLTG	----	QWHDGNTFTIFLL	:	59		
	*	200	*	22	*	240	*	260						
ATPT2	:	AVFAALMNNIYIVG	ENQISDVEHDKVNKPYLPLASGEYSVNTGIAIVASFSTMSFWLGIWGSWPLFWALFVSFMLGTAYS	INIPPLR	:	228								
SLR1736	:	AWFACLLGNVYIVG	ENQIMDVHIDRINKPNLPLANGDFSIAQGRWLVGLCGVASFAIAFWGLG	LWLGLTVGSLIIGTAY	----	SVPPVR	:	134						
ATPT3	:	GALL	----	IRGAGCTINDLQDIDTKVDRTKLRDPIASGLHT	----	PFOGIGFICQLLGLG	----	ILLQNNYSRVLGAS	----	SLILVIF	:	246		
SLR0926	:	GTHA	----	TSLGCVVNDLMDRDIDPOVERTKQRLAARMS	----	VQVGIGVAVALLCAG	----	LAFFILTPFSFWLCVA	----	AVPVIV	:	132		
ATPT4	:	TMMI	----	AASANSNQIEISNDSKMKRTMLRPLPSGRSVPHAVAWATHAGSACL	----	LAASKTNMBAAGLASAN	----	LVLVAF	:	215				
SLL1899	:	GTHA	----	AASAQTNCLYQDIDYEMLRTRARPIPAKQVQPHALIFALATGVTSFAL	----	LAFTFVNVLSCGLALSG	----	IVFYML	:	137				
ATPT12	:	MMMSGPCITGYTOTINDWDRDIDDAINEPYRPI	ESGAISEPEVITQVWVLGGGIGIAGILD	VWAGHTTPTVFYALG	----	GSLISY	:	223						
SLR0056	:	MLPSGPLMTGYTOTINDFYDRDIDDAINEPYRPI	ESGAISVPQVVTQILLILEVAGIGVAYGLD	VWAQHDFFPMVMTLIG	----	GAFVAY	:	157						
ATPT8	:	GIAE	----	ITEMIHVASLTHDDVLDDADTRGVGSLNVVMGNKMSVLAGDFL	SRACGAL	----	AALKNTEVVALLATAVEHLVTGETM	:	144					
SLR1518	:	SATA	----	IAWINLSNDFVDSDTGIDVRKAHSVNLGTGRNRLVFLISNFFEL	AGLGLMSMS	----	WRAQDWTVLELIGVA	----	IFLGY	:	138			
		n	d	d										

Figure 22A



ATPT2	WKR-FALVAAMCILA	RAII	QIAFYEH-IQTHVFG	RPIIFTRP	PLIFATAFMS	FFSVVIA	FKDIPDIE	GDKI-FG	FRSFSVTLG-QKR	313																																																																			
SLR1736	LKR-FSLAALCIL	TVRGIVN	GLFDF-FRIGLGY	PPPTITPT	IMV-LTLFIL	FAVAIAIA	FKDVPDME	GDRQ-FKQ	QTEITLQIG-KQN	218																																																																			
ATPT3	SMP-LMKRFTFP	QAFGLT	TNNWGLG--WT--	AVKGS	LAPSIL	PLYL	SGVCMV	YYDTIY	AHQDKEDDVK-VGV	KSTALRFG-DNT	328																																																																		
SLR0926	AMP-GAKRFP	VPQLVLS	IAWGFAYLS--WS--	AVTGD	TDATWV-LWG	ATVFTW	FGDTVY	AMADRED	RR-FCWN	SSALFFG-QYV	213																																																																		
ATPT4	VMT-PLKQ	LHPINTW	GAVVGAIP	PLG--WA--	AASQ	SYNSMI-LPA	ALYFQ	PHFMA	LALCRNDYAA-CGY	KMSLFD	294																																																																		
SLR1899	VYTHW	LKRHTAQ	NIIVIGGA	AGSIP	PLG--WA--	AVTGD	LSWTPWV-LF	ALIFL	MPPHFW	ALALMIKDDYAO-VNV	PMIPVIA	220																																																																	
ATPT12	INS-APPL	KLKQNGW	GNFAG	ASYLSLP	WAGQAL	FGTIP	DDVVV-LT	LYSIAG	CIANV	DFKSVEG	DRALCL	QSLP	VAFG-TET	308																																																															
SLR0056	INS-APPL	KLKQNGW	GNFAG	ASYLSLP	WAGQAL	FGTIP	DDVVV-LT	LYSIAG	CIANV	DFKSVEG	DRALCL	QSLP	VAFG-TET	308																																																															
ATPT8	EITS	STEQRYSMDYY	QKTY	YKTAS	INS	CKAVAV	LTGQ	AEVAV	LAFEY	GRNLG	AFQ	IDD	ILDT	GT	SASLCKG	SLSDIRH--GV	231																																																												
SLR1518	TS	QGP	PPRLGLGL	GELICL	ITFG	DAI-AAAY	SQS	SFWN	LT-PSV	FVGIS	AILF	CSHF	HQV	DDLA-AG	KKSP	IVRLG-TKL	223																																																												
ATPT2	VF	WTCV	TLQ	MAYANA	IAIV	GATSP	FIWSK	VISV	GHV	IAIT	WARAK	SVDL	SSKTE	ITS--CYM	IWK	FV	AEY	MLPFLK----	393																																																										
SLR1736	VFR	GT	ILL	TCYL	AMAM	WG	WA	AMPL	NTAF	IV	SHL	CLAL	WRS	RDVH	LES	TE	IAS--FYQ	IWK	FLEY	MLYPLALWLP	NFS	304																																																							
ATPT3	KL	WT	TG	FTAS	IG	FTAL	SG	FAD	LQWQ	YAS	MAA	SG	QWQ	GT	ADL	SSG	ADCS--RKE	VSN	KWFG	ATG	IFSG	VLR	SFQ--	407																																																					
SLR0926	GEA	V	G	FF	ALT	IG	CF	Y	GM	MLN	PLY	WLS	LA	TA	---	VGW	YQ	I	Q	L	S	A	P	T	P	E	P	--K	Y	---	GQ	I	G	Q	N	I	I	G	F	V	L	E	A	G	N	L	G	W	L	---	292																										
ATPT4	GK	R	AA	V	A	R	N	C	F	Y	M	I	P	E	G	F	A	Y	D	W	L	T	S	S	W	F	C	E	S	T	L	T	L	A	---	AA	T	A	F	S	F	R	D	R	T	H	K	A	---	R	K	M	E	H	A	S	I	L	P	V	F	M	S	G	L	L	H	R	V	S	N	D	---	379			
SLR1899	V	S	Q	I	W	Y	S	L	V	V	P	F	S	L	L	V	P	L	H	Q	L	G	I	L	Y	L	A	T	A	---	G	G	O	F	I	V	K	A	W	Q	L	K	A	P	G	R	D	D	I	A	---	R	G	L	E	K	F	S	I	F	I	M	L	L	C	L	A	M	V	D	S	L	P	V	T	---	303
ATPT12	A	K	W	I	C	G	A	I	D	I	T	Q	L	S	V	A	G	Y	L	A	S	K	P	Y	A	L	A	V	A	---	E	P	O	I	V	F	Q	F	K	Y	L	K	D	P	V	K	D	V	K	---	Y	O	A	S	A	Q	P	F	L	V	L	G	I	F	V	T	A	L	A	S	Q	H	---	387			
SLR0056	A	A	W	I	C	G	A	I	D	I	T	Q	L	S	V	A	G	Y	L	A	S	K	P	Y	A	L	A	V	A	---	E	P	O	I	V	F	Q	F	K	Y	L	K	D	P	V	K	D	V	K	---	Y	O	A	S	A	Q	P	F	L	V	L	G	I	F	V	T	A	L	A	S	Q	H	---	387			
ATPT8	I	T	A	P	I	E	F	A	N	E	E	F	P	Q	I	R	E	V	D	Q	E	K	D	P	R	N	V	I	A	E	---	E	P	O	I	V	F	Q	F	K	Y	L	K	D	P	V	K	D	V	K	---	Y	O	A	S	A	Q	P	F	L	V	L	G	I	F	V	T	A	L	A	S	Q	H	---	387		
SLR1518	G	S	Q	I	W	Y	S	L	V	V	P	F	S	L	L	V	P	L	H	Q	L	G	I	L	Y	L	A	T	A	---	G	G	O	F	I	V	K	A	W	Q	L	K	A	P	G	R	D	D	I	A	---	R	G	L	E	K	F	S	I	F	I	M	L	L	C	L	A	M	V	D	S	L	P	V	T	---	303
ATPT2	VF	WTCV	TLQ	MAYANA	IAIV	GATSP	FIWSK	VISV	GHV	IAIT	WARAK	SVDL	SSKTE	ITS--CYM	IWK	FV	AEY	MLPFLK----	393																																																										
SLR1736	VFR	GT	ILL	TCYL	AMAM	WG	WA	AMPL	NTAF	IV	SHL	CLAL	WRS	RDVH	LES	TE	IAS--FYQ	IWK	FLEY	MLYPLALWLP	NFS	304																																																							
ATPT3	KL	WT	TG	FTAS	IG	FTAL	SG	FAD	LQWQ	YAS	MAA	SG	QWQ	GT	ADL	SSG	ADCS--RKE	VSN	KWFG	ATG	IFSG	VLR	SFQ--	407																																																					
SLR0926	GEA	V	G	FF	ALT	IG	CF	Y	GM	MLN	PLY	WLS	LA	TA	---	VGW	YQ	I	Q	L	S	A	P	T	P	E	P	--K	Y	---	GQ	I	G	Q	N	I	I	G	F	V	L	E	A	G	N	L	G	W	L	---	292																										
ATPT4	GK	R	AA	V	A	R	N	C	F	Y	M	I	P	E	G	F	A	Y	D	W	L	T	S	S	W	F	C	E	S	T	L	T	L	A	---	AA	T	A	F	S	F	R	D	R	T	H	K	A	---	R	K	M	E	H	A	S	I	L	P	V	F	M	S	G	L	L	H	R	V	S	N	D	---	379			
SLR1899	V	S	Q	I	W	Y	S	L	V	V	P	F	S	L	L	V	P	L	H	Q	L	G	I	L	Y	L	A	T	A	---	G	G	O	F	I	V	K	A	W	Q	L	K	A	P	G	R	D	D	I	A	---	R	G	L	E	K	F	S	I	F	I	M	L	L	C	L	A	M	V	D	S	L	P	V	T	---	303
ATPT12	A	K	W	I	C	G	A	I	D	I	T	Q	L	S	V	A	G	Y	L	A	S	K	P	Y	A	L	A	V	A	---	E	P	O	I	V	F	Q	F	K	Y	L	K	D	P	V	K	D	V	K	---	Y	O	A	S	A	Q	P	F	L	V	L	G	I	F	V	T	A	L	A	S	Q	H	---	387			
SLR0056	A	A	W	I	C	G	A	I	D	I	T	Q	L	S	V	A	G	Y	L	A	S	K	P	Y	A	L	A	V	A	---	E	P	O	I	V	F	Q	F	K	Y	L	K	D	P	V	K	D	V	K	---	Y	O	A	S	A	Q	P	F	L	V	L	G	I	F	V	T	A	L	A	S	Q	H	---	387			
ATPT8	I	T	A	P	I	E	F	A	N	E	E	F	P	Q	I	R	E	V	D	Q	E	K	D	P	R	N	V	I	A	E	---	E	P	O	I	V	F	Q	F	K	Y	L	K	D	P	V	K	D	V	K	---	Y	O	A	S	A	Q	P	F	L	V	L	G	I	F	V	T	A	L	A	S	Q	H	---	387		
SLR1518	G	S	Q	I	W	Y	S	L	V	V	P	F	S	L	L	V	P	L	H	Q	L	G	I	L	Y	L	A	T	A	---	G	G	O	F	I	V	K	A	W	Q	L	K	A	P	G	R	D	D	I	A	---	R	G	L	E	K	F	S	I	F	I	M	L	L	C	L	A	M	V	D	S	L	P	V	T	---	303
ATPT2	VF	WTCV	TLQ	MAYANA	IAIV	GATSP	FIWSK	VISV	GHV	IAIT	WARAK	SVDL	SSKTE	ITS--CYM	IWK	FV	AEY	MLPFLK----	393																																																										
SLR1736	VFR	GT	ILL	TCYL	AMAM	WG	WA	AMPL	NTAF	IV	SHL	CLAL	WRS	RDVH	LES	TE	IAS--FYQ	IWK	FLEY	MLYPLALWLP	NFS	304																																																							
ATPT3	KL	WT	TG	FTAS	IG	FTAL	SG	FAD	LQWQ	YAS	MAA	SG	QWQ	GT	ADL	SSG	ADCS--RKE	VSN	KWFG	ATG	IFSG	VLR	SFQ--	407																																																					
SLR0926	GEA	V	G	FF	ALT	IG	CF	Y	GM	MLN	PLY	WLS	LA	TA	---	VGW	YQ	I	Q	L	S	A	P	T	P	E	P	--K	Y	---	GQ	I	G	Q	N	I	I	G	F	V	L	E	A	G	N	L	G	W	L	---	292																										
ATPT4	GK	R	AA	V	A	R	N	C	F	Y	M	I	P	E	G	F	A	Y	D	W	L	T	S	S	W	F	C	E	S	T	L	T	L	A	---	AA	T	A	F	S	F	R	D	R	T	H	K	A	---	R	K	M	E	H	A	S	I	L	P	V	F	M	S	G	L	L	H	R	V	S	N	D	---	379			
SLR1899	V	S	Q	I	W	Y	S	L	V	V	P	F	S	L	L	V	P	L	H	Q	L	G	I	L	Y	L	A	T	A	---	G	G	O	F	I	V	K	A	W	Q	L	K	A	P	G	R	D	D	I	A	---	R	G	L	E	K	F	S	I	F	I	M	L	L	C	L	A	M	V	D	S	L	P	V	T	---	303
ATPT12	A	K	W	I	C	G	A	I	D	I	T	Q	L	S	V	A	G	Y	L	A	S	K	P	Y	A	L	A	V	A	---	E	P	O	I	V	F	Q	F	K	Y	L	K	D	P	V	K	D	V	K	---	Y	O	A	S	A	Q	P	F	L	V	L	G	I	F	V	T	A	L	A	S	Q	H	---	387			
SLR0056	A	A	W	I	C	G	A	I	D	I	T	Q	L	S	V	A	G	Y	L	A	S	K	P	Y	A	L	A	V	A	---	E	P	O	I	V	F	Q	F	K	Y	L	K	D	P	V	K	D	V	K	---	Y	O	A	S	A	Q	P	F	L	V	L	G	I	F	V	T	A	L	A	S	Q	H	---	387			
ATPT8	I	T	A	P	I	E	F	A	N	E	E	F	P	Q	I	R	E	V	D	Q	E	K	D	P	R	N	V	I	A	E	---	E	P	O	I	V	F	Q	F	K	Y	L	K	D	P	V	K	D	V	K	---	Y	O	A	S	A	Q	P	F	L	V	L	G	I	F	V	T	A	L	A	S	Q	H	---	387		
SLR1518	G	S	Q	I	W	Y	S	L	V	V	P	F	S	L	L	V	P	L	H	Q	L	G	I	L	Y	L	A	T	A	---	G	G	O	F	I	V	K	A	W	Q	L	K	A	P	G	R	D	D	I	A	---	R	G	L	E	K	F	S	I	F	I	M	L	L	C	L	A	M	V	D	S	L	P	V	T	---	303
ATPT2	VF	WTCV	TLQ	MAYANA	IAIV	GATSP	FIWSK	VISV	GHV	IAIT	WARAK	SVDL	SSKTE	ITS--CYM	IWK	FV	AEY	MLPFLK----	393																																																										
SLR1736	VFR	GT	ILL	TCYL	AMAM	WG	WA	AMPL	NTAF	IV	SHL	CLAL	WRS	RDVH	LES	TE	IAS--FYQ	IWK	FLEY	MLYPLALWLP	NFS	304																																																							
ATPT3	KL	WT	TG	FTAS	IG	FTAL	SG	FAD	LQWQ	YAS	MAA	SG	QWQ	GT	ADL	SSG	ADCS--RKE	VSN	KWFG	ATG	IFSG	VLR	SFQ--	407																																																					
SLR0926	GEA	V	G	FF	ALT	IG	CF	Y	GM	MLN	PLY	WLS	LA	TA	---	VGW	YQ	I	Q	L	S	A	P	T	P	E	P	--K	Y	---	GQ	I	G	Q	N	I	I	G	F	V	L	E	A	G	N	L	G	W	L	---	292																										
ATPT4	GK	R	AA	V	A	R	N	C	F	Y	M	I	P	E	G	F	A	Y	D	W	L	T	S	S	W	F	C	E	S	T	L	T	L	A	---	AA	T	A	F	S	F	R	D	R	T	H	K	A	---	R	K	M	E	H	A	S	I	L	P	V	F	M	S	G	L	L	H	R	V	S	N	D	---	379			
SLR1899	V	S	Q	I	W	Y	S	L	V	V	P	F	S	L	L																																																														



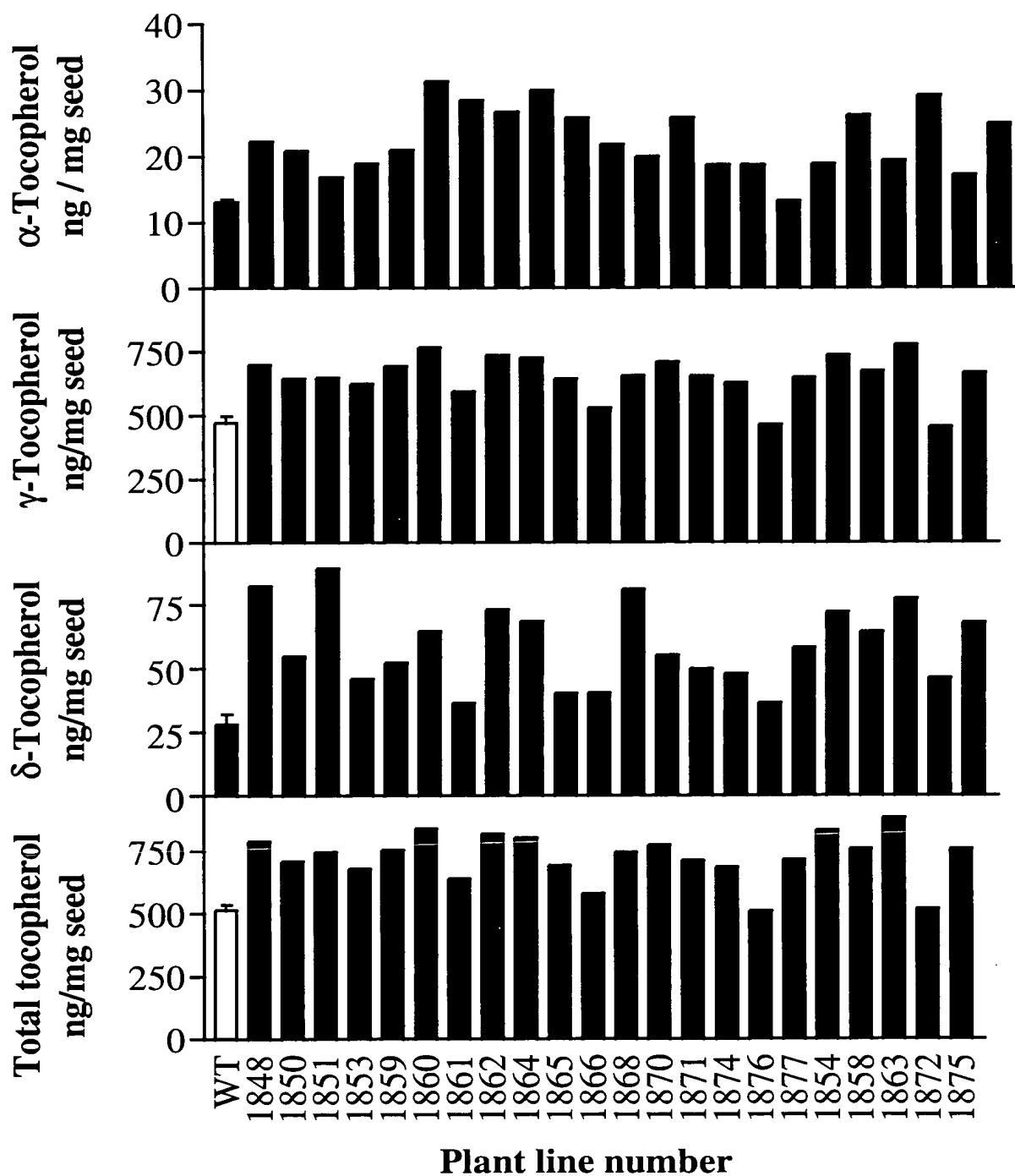


Figure 24

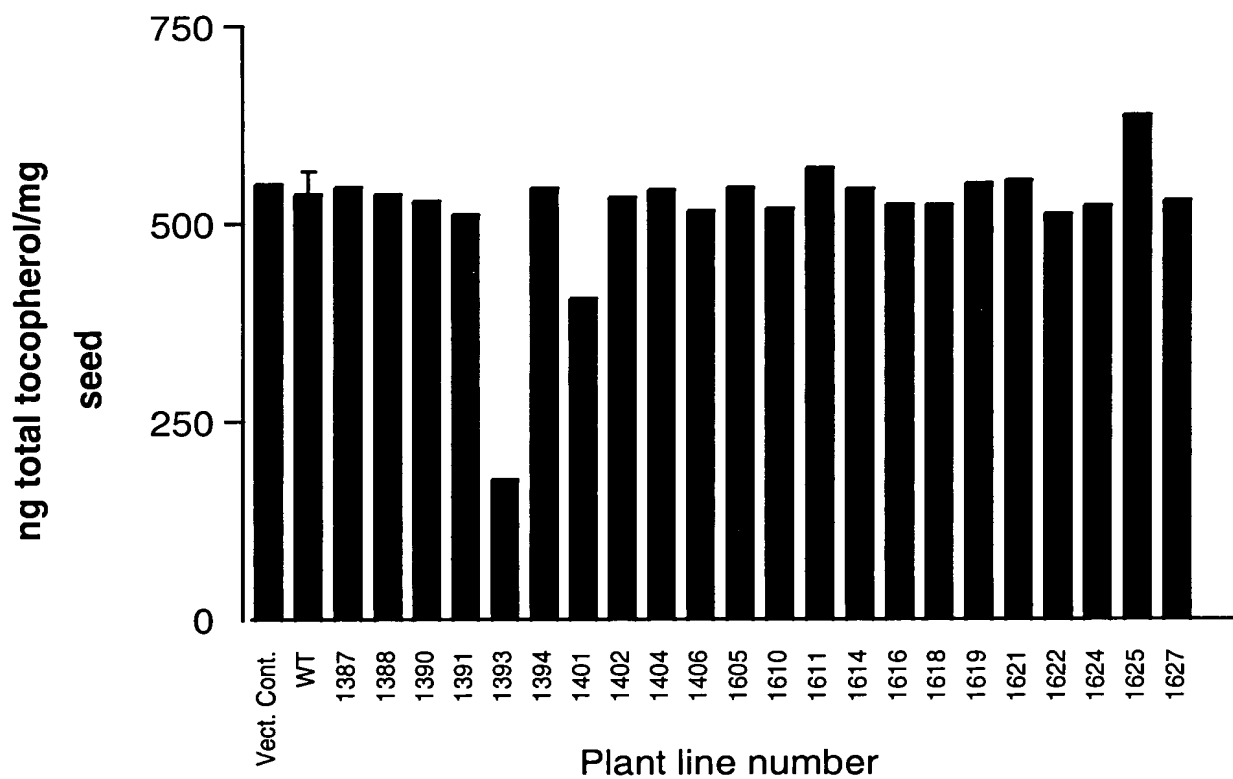


Figure 25

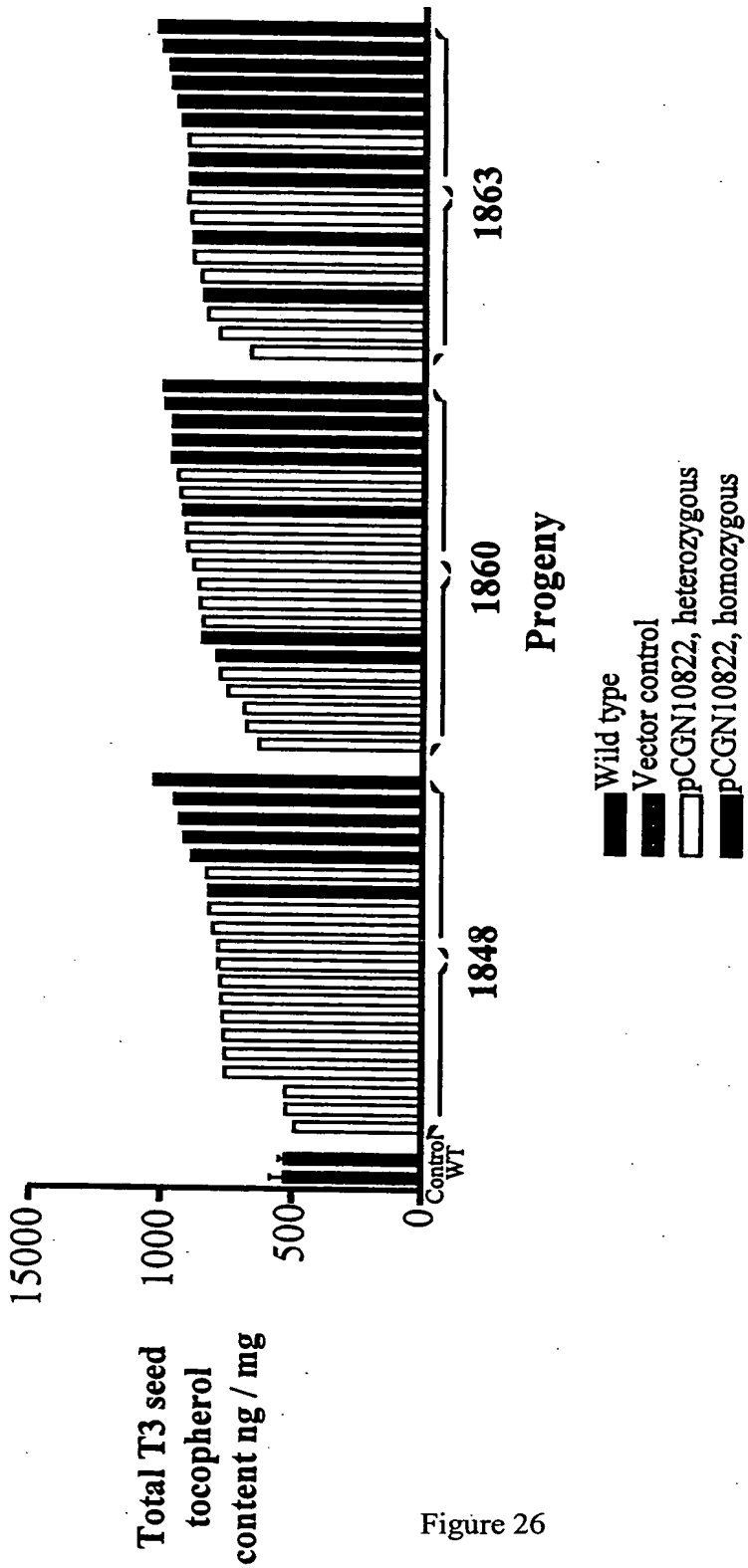


Figure 26

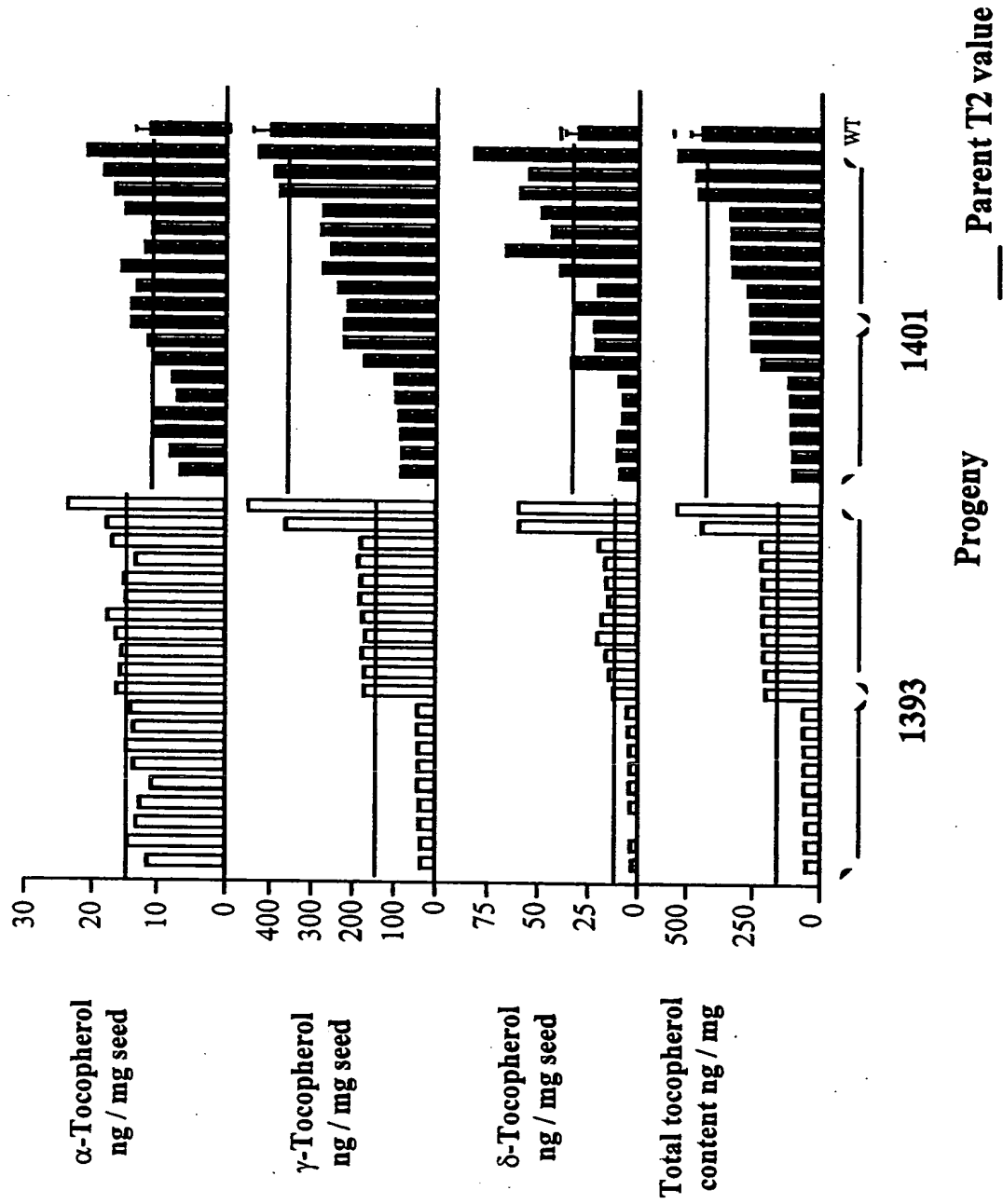


Figure 27



Total tocopherol in Napin ATPT2 Canola Seed

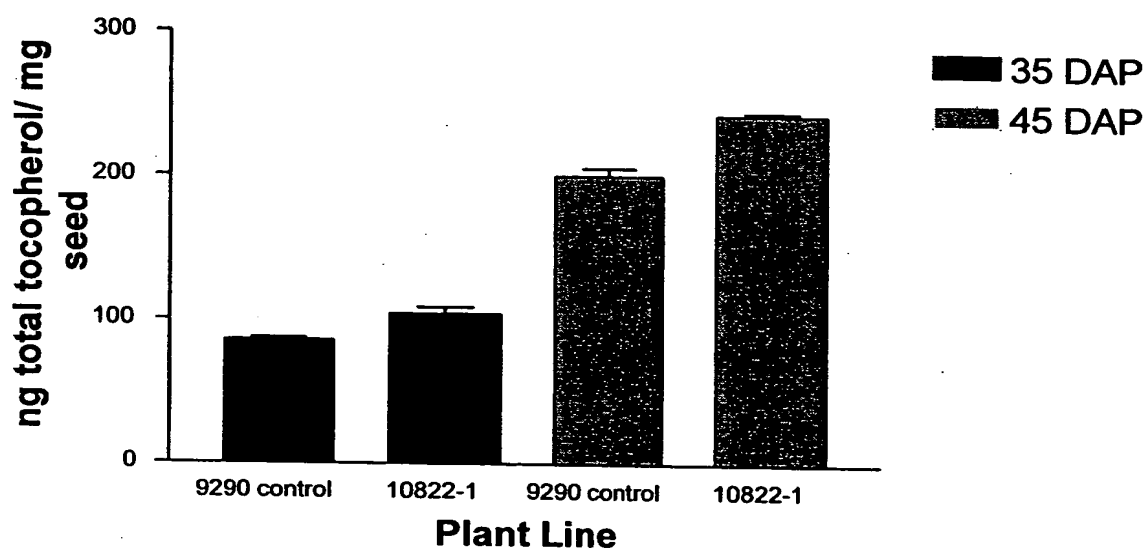


Figure 28

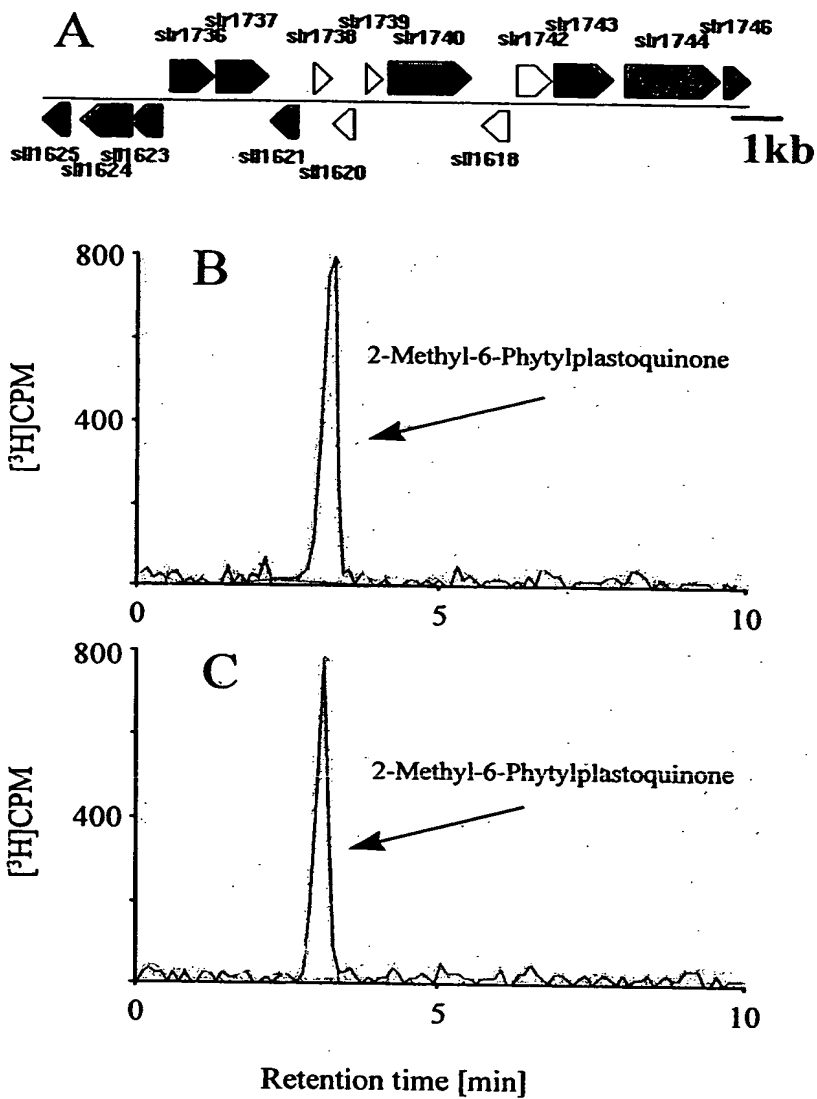


Figure 29

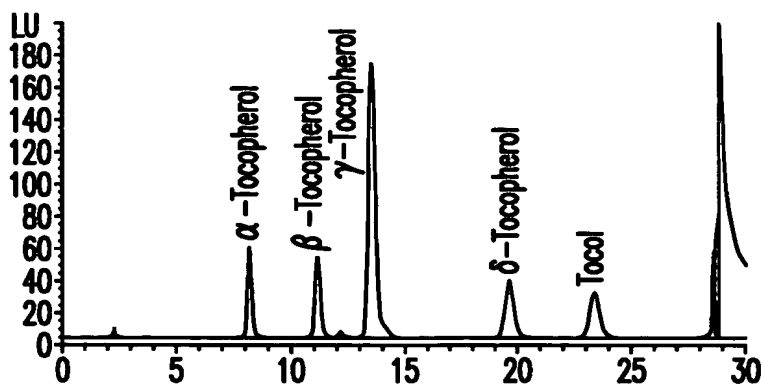
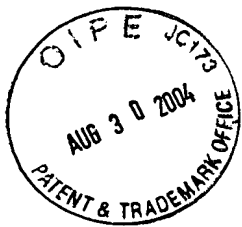


Figure 30A

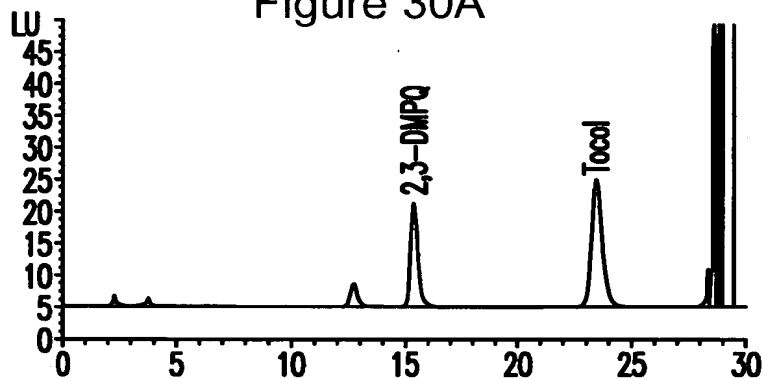


Figure 30B

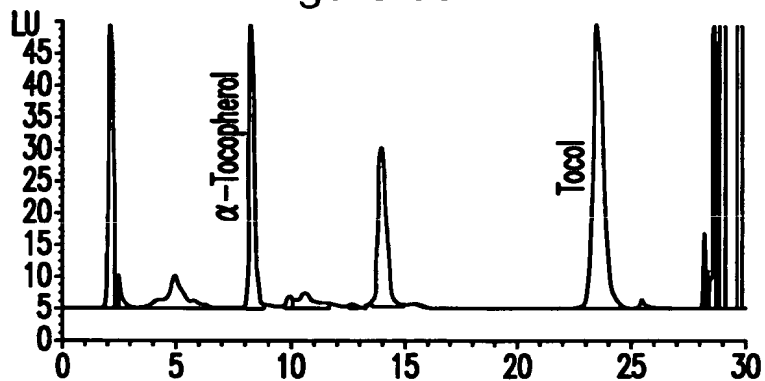


Figure 30C

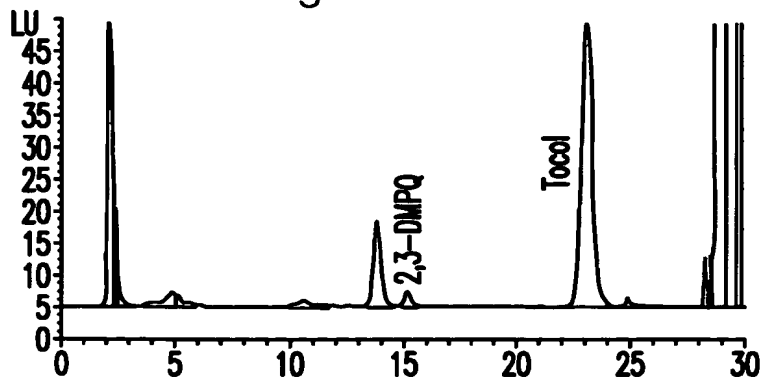


Figure 30D

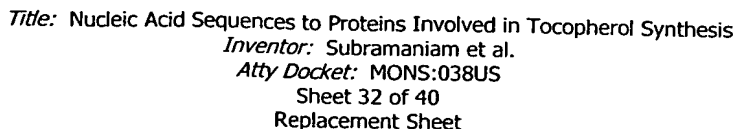


Figure 31A



Query- 11475 AGAGAAGAGGGAGAGTTTTTGTTTTATGTATTCTGTGGAGAATCCTGCATTTCCGGCAGAG
ATCEA4C371+ 362 AGAGAAGAGGGAGAGTTTTTGTTTTATGTATTCTGTGGAGAATCCTGCATTTCCGGCAGAG
PIR:T04448 46 E K R E S F C F M Y S V E N P A F R Q S

Query- 11415 TTTGTCACCATTGGAAGTGGCTCTATATGGACCTAGATTCACTGGTGTGGAGCTCAGAT
ATCEA4C371+ 422 TTTGTCACCATTGGAAGTGGCTCTATATGGACCTAGATTCACTGGTGTGGAGCTCAGAT
PIR:T04448 66 L S P L E V A L Y G P R F T G V G A Q I

Query- 11355 TCTTGGCGCTAATGATAAATATTTATGCCAATACGAACAAGACTCTCACAATTTCTGGGG
ATCEA4C371+ 482 TCTTGGCGCTAATGATAAATATTTATGCCAATACGAACAAGACTCTCACAATTTCT
PIR:T04448 86 L G A N D K Y L C Q Y E Q D S H N F W G
ATCEA4C371+ Exon 11538 11301 Confidence: 100 100

Query- 11295 AGGTAACCTCCTTGACCCTTAAAATGCTGTGTCATGACAATAAGAAATCATATCTGAGTCT
ATCEA4C371+ 537
PIR:T04448 106 D
PIR:T04448 Exon 11609 11294 Confidence: 100 100

Query- 11235 TTTCTCTACTTCTAGTACTAATGTTTCGTTATTGTTGTTAAAGATCTAAGTCTTATCTGAA
PIR:T04448 107

Query- 11175 TTTTGTTACATTTTGGTTCCTGGTGCCTTCTCAACATGAATTTGTATATATGACTTTTAAAG
PIR:T04448 107

Query- 11115 ATTGCTTACCTAAAGTTTTTACTCATGCATAGATCGACATGAGCTAGTTTGGGGAATAC
PIR:T04448 107 R H E L V L G N T

Query- 11055 TTTTAGTGCTGTGCCAGGCGCAAAGGCTCCAAACAAGGAGGTTCCACCAGAGGTTCTCAC
PIR:T04448 116 F S A V P G A K A P N K E V P P E
PIR:T04448 Exon 11083 11004 Confidence: 96 100

Query- 10995 TCCTCCCTTGTTGGTTACTTTGTTATCTGTTAAATAGTTTCCAATTGTATCCGGATAGT
PIR:T04448 133

Query- 10935 GTTCTACTTCTCCTTGTAGAAAATCTCAAGTTTTTGTACTCTTGCTATTCTCTGGATG
PIR:T04448 133

Query- 10875 TTGATTTGTAAAGCATGTCGTTTTATTGTAGGAATTTAACAGAAGAGTGTCGAAGGGTT
PIR:T04448 133 E F N R R V S E G F

Query- 10815 CCAAGCTACTCCATTTTGGCATCAAGGTCACATTTGCGATGATGGCCGGTAATTATATGA
PIR:T04448 143 Q A T P F W H Q G H I C D D G R
PIR:T04448 Exon 10844 10768 Confidence: 100 100

Query- 10755 TTCTATGCACAACAAGAATTCATATATTATAAATATTGGATATTGAGTATTTTTGTTGA
PIR:T04448 159

Figure 31B



Query- 10635 TGAAATCTGCTCGTTGGGAGTATAGTACTCGTCCCGTTTACGGTTGGGGTGATGTTGGGG
PIR:T04448 166 K S A R W E Y S T R P V Y G W G D V G A

Query- 10575 CCAAACAGAAGTCAACTGCAGGCTGGCCTGCAGCTTTTCCTGTATTGAGCCTCATTGGC
PIR:T04448 186 K Q K S T A G W P A A F P V F E P H W Q

Query- 10515 AGATATGCATGGCAGGAGGCCTTTCCACAGGTGTGAGCTTTGCTTGATTGACTTAAAGTT
PIR:T04448 206 I C M A G G L S T G
PIR:T04448 Exon 10655 10486 Confidence: 96 100

Query- 10455 AATAAATAGACGGTTAAGTTTACTTGCCTAGTACTAACAGAAAATTAAGAAAGAAACCAC
PIR:T04448 216

Query- 10395 CCTCTTTCTATCAGCAGAACTGCTATTGTAGTTCTTATTTTCTCTTGTATTGTCAGG
PIR:T04448 216

Query- 10335 GTGGATAGAATGGGGCGGTGAAAGGTTTGAGTTTCGGGATGCACCTTCTTATTCAGAGAA
PIR:T04448 216 W I E W G G E R F E F R D A P S Y S E K

Query- 10275 GAATTGGGGTGGAGGCTTCCCAAGAAAATGGTTTGGGTAAAACATTTTCATCCTTTTGCT
PIR:T04448 236 N W G G G F P R K W F W
PIR:T04448 Exon 10336 10239 Confidence: 96 100

Query- 10215 ACATTTCTTGTTGCAGACTTTAGTTAGCTAGTGGACCTGTGTATACACCCACATGTAGTA
PIR:T04448 248

Query- 10155 TACTTGTGTTGATAGCTTTATTTGTCAATGTCTCTTTACAGGTCCAGTGAATGTCTTTGA
PIR:T04448 248 V Q C N V F E

Query- 10095 AGGGGCAACTGGAGAAGTTGCTTTAACCGCAGGTGGCGGGTTGAGGCAATTGCCTGGATT
PIR:T04448 255 G A T G E V A L T A G G G L R Q L P G L

Query- 10035 GACTGAGACCTATGAAAATGCTGCACTGGTATGCACTTATAAGATCTTCTTAAGCAATGA
PIR:T04448 275 T E T Y E N A A L
PIR:T04448 Exon 10115 10008 Confidence: 100 100

Query- 9975 CAGTGAGTATTAGAAGGCAGATAGTTTACAAAAGCTCTGGGCCCTTGTAATCTGCAGGT
PIR:T04448 284 V

Query- 9915 TTGTGTACACTATGATGGAAAAATGTACGAGTTTGTTCCTTGAATGGTGTGTTAGATG
PIR:T04448 285 C V H Y D G K M Y E F V P W N G V V R W
GSDB:S:495- 532 tagatg

Figure 31C



Title: Nucleic Acid Sequences to Proteins Involved in Tocopherol Synthesis

Inventor: Subramaniam et al.

Atty Docket: MONS:038US

Sheet 36 of 40

Replacement Sheet

Query- 9436 AAAGAGCTCAATGGCAGCAGTGGAGATAGGAGGAGGACCGTGGTTTGGGACATGGAAAGG
PIR:T04448 402 K S S M A A V E I G G G P W F G T W K G
GSDB:S:495- 307 aaagagctcaatggcaNcagtggagataggaggaggaccgtggtttgggacatggaaagg

Query- 9376 AGATACGAGCAACACGCCCGAGCTACTAAAACAGGCTCTTCAGGTCCCATTGGATCTTGA
PIR:T04448 422 D T S N T P E L L K Q A L Q V P L D L E
GSDB:S:495- 247 agatacgagcaacacgcccagactactaaaacaggctcttcaggtcccattggatcttga

Query- 9316 AAGCGCCTTAGGTTTGGTCCCTTTCTTCAAGCCACCGGGTCTGTAA
(stop)
PIR:T04448 442 S A L G L V P F F K P P G L
GSDB:S:495- 187 aagcgccttaggtttgggtccctttcttcaagccaccgggtctgtaacattgatgagtgtt
PIR:T04448 Exon 9522 9274 Confidence: 100 100

Query- 9256
PIR:T04448 456
GSDB:S:495- 127 ttgtttgttgatagagaccatgtgatgaatgaagccttagtcatgtcattgctagcttc

Query- 9196 ACTATTATGTATGTATGATTTTAGTTCGTTTCGGTCCTTGTGGTAAATGATACGGGCCAGT
GSDB:S:495- 67 actattatgtatgtatgatttttagttcgttcgggtccttgtggtaaataatgatacgggccagt

Query- 9136 GTAAAGTCTAGTTCAATAAAAGCCTTGAGTCGCATAATTTCAATTCAAATTGCATC
GSDB:S:495- 7 gtaaagt
GSDB:S:495- Exon 9450 9130 Confidence: 98 100

ATCEA4C37145_1 3063693/emb|CAA18584.1| 4.0e-43 (AL022537) putative protein
[Arabidopsis thaliana]

PIR:T04448 sPIR-T04448 shypothetical protein F4D11.30 - Arabidopsis thaliana;
g3063693|emb|CAA18584.1 (AL022537) putative protein [Arabidopsis thaliana]_F4D11.30

GSDB:S:4955486|AI995392|AI995392|701673779 A. thaliana, Columbia Col-0, inflorescence-
1 Arabidopsis thaliana cDNA clone 701673779, mRNA sequence.

Figure 31E

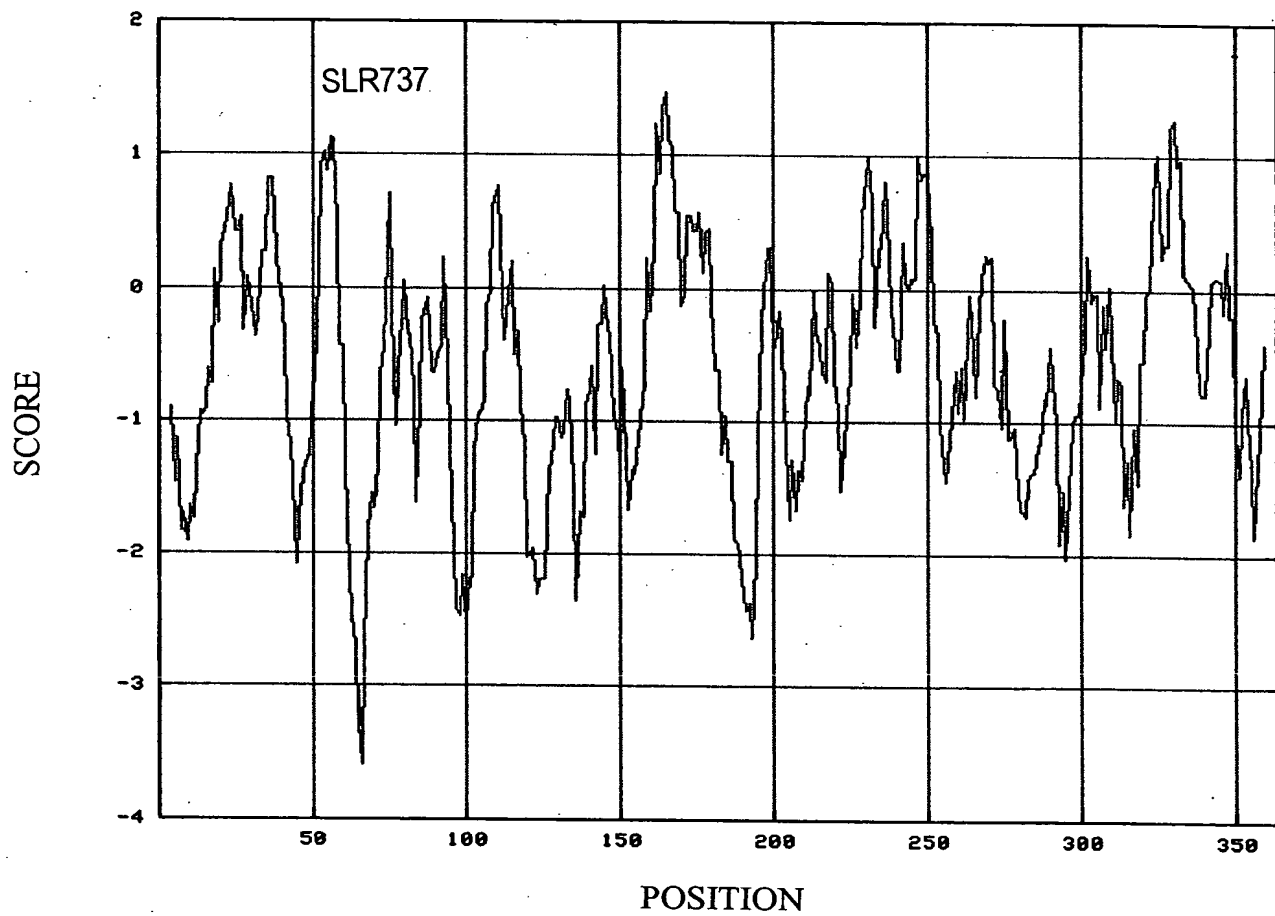


Figure 32

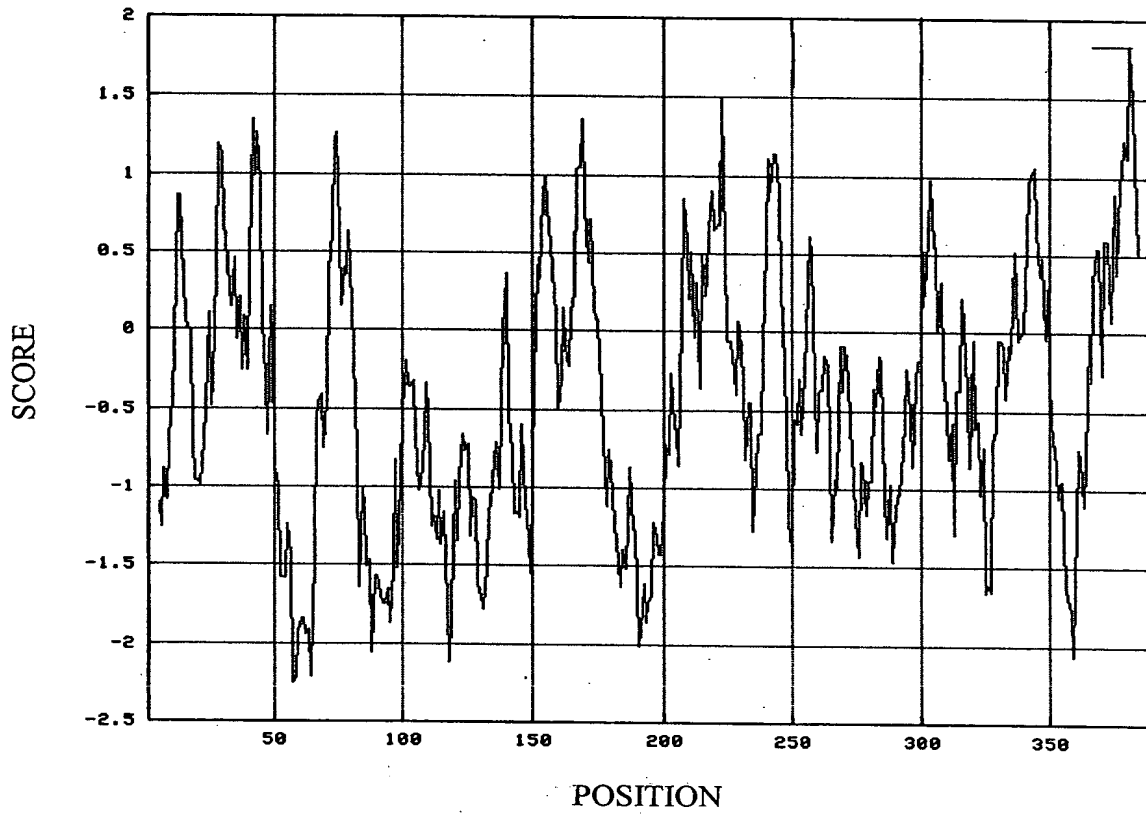


Figure 33

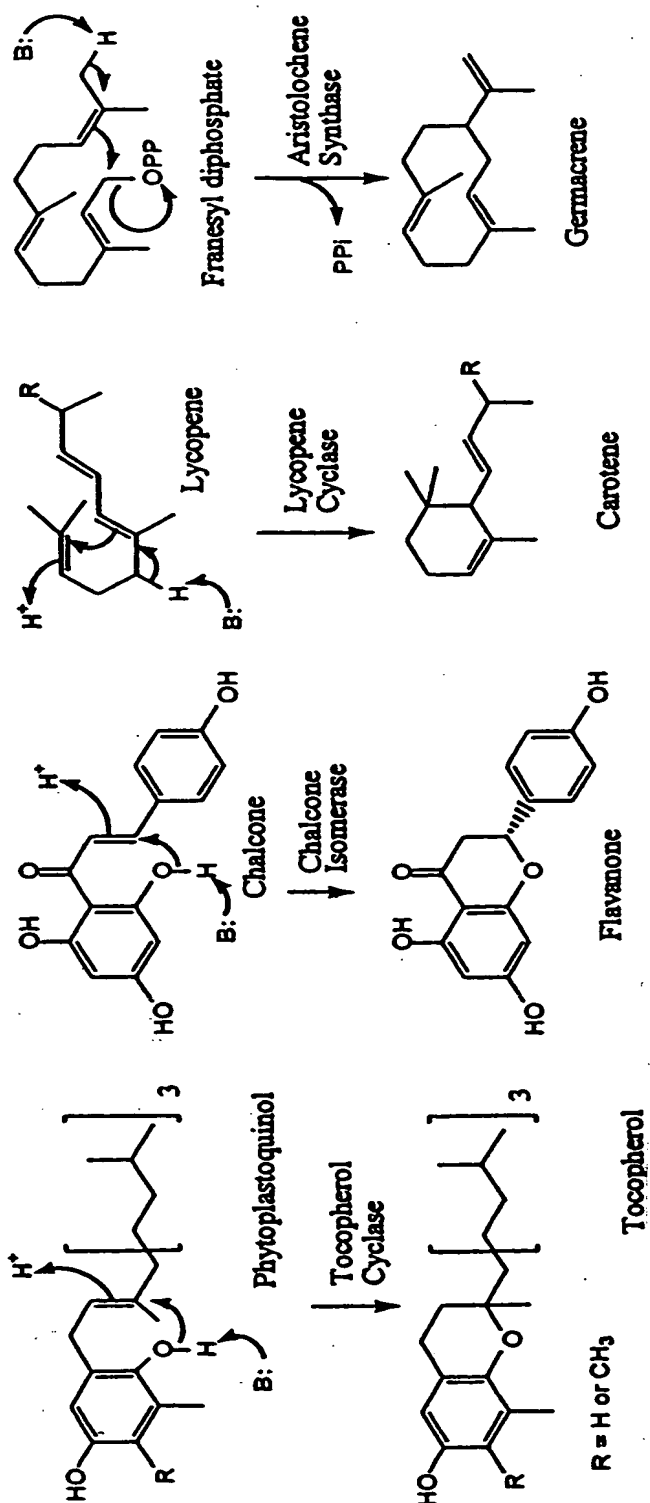


Figure 34



slr1737_SYNSP_S74814_
 slr1737_ARATH_T04448_
 CFI_ARATH_P41088_

slr1737_SYNSP_S74814_
 slr1737_ARATH_T04448_
 CFI_ARATH_P41088_

slr1737_SYNSP_S74814_
 slr1737_ARATH_T04448_
 CFI_ARATH_P41088_

slr1737_SYNSP_S74814_
 slr1737_ARATH_T04448_
 CFI_ARATH_P41088_

slr1737_SYNSP_S74814_
 slr1737_ARATH_T04448_
 CFI_ARATH_P41088_

slr1737_SYNSP_S74814_
 slr1737_ARATH_T04448_
 CFI_ARATH_P41088_

slr1737_SYNSP_S74814_
 slr1737_ARATH_T04448_
 CFI_ARATH_P41088_

slr1737_SYNSP_S74814_
 slr1737_ARATH_T04448_
 CFI_ARATH_P41088_

slr1737_SYNSP_S74814_
 slr1737_ARATH_T04448_
 CFI_ARATH_P41088_

slr1737_SYNSP_S74814_
 slr1737_ARATH_T04448_
 CFI_ARATH_P41088_

-----M
 MEIRSLIVSMNPNLSSFELSRPVSPLTRSLVPFRSTKLVPRSISRVSASI

KFP-----PHSGYHWQGS-PFFEGWYVRL
 STPNSETDKISVKPVYVPTSPNRELRTPHSGYHFDGTPRKFFEGWYFRVS

LPOSGESFAFMYSIENPASDHYYGGGAVQILGPATK----KQENQEDQLV
 IPEKRESFCFMYSVENPAFRQSLSPLEVALYGPRTGVGAQILGANDKYL
 MSSSNACASPSPPFA----VTKLHVDSV-

WRTFPSVKKFWASPROFALG-HWGKCRDNRQ-AKPLLSEEFFATVKEGYQ
 CQYEQDSHNFWDGRHELVLGNTFSAPVGAAPNKEVPPEEFNRRVSEGFO
 --TFVPSVKSPASSNPLFLG-GAGVRGLDIQ-GK-----FVIFTVIGVY

IHQNHQGGIHHGDR-----HCRWQFTVEPEVTWGSNRFPRATAGW
 ATPFWHQGHICDDGRTDYAETVKSARWEYSTRPVYWGWDVGAKQKSTAGW
 LEGNAVPSLSV-----KWKGKTEELTESIPFFREIVTGA

LSFLPLFDPGWQILLAQGRAHGWLKWQREQYEFDHALVYAEKNWGHSPFP
 PAAFPVFEPHWQICMAGGLSTGWIEWGGERFEFRDAPSYSEKNWGGGFPR
 EKFIKVT-----M-----KLPLTGQQYSEKVTENC

RWFWLQANYFPDHPG-LSVTAAGGERIVLGRPE---EVALIGLHHQGNFY
 KWFVWQCNVFEAGTGEVALTAGGGLRQLPGLTETYEALVCVHYDGKMY
 VAIWKQLGLYTDCEA-KAV-----EKFLEIFKE---ET-----

EFPGHGTVTWQVAPWGRWQLKASNDRYWVKLSGKTDKKGSLVHTP-TAQ
 EFVPWNGVVRWEMSPWGYWYITAENENHVVELEARTNEAGTPLRAPTEV
 -FPPG-SSILFALSPTGSLTVAFSKDDS-IPETGIAVIENKLLAEA-VLE

GLQLNCRDTRGYLYLQGSVGHG-----LIVQGETDTAGLEVGG-----
 GLATACRDSCYELKLQIWERLYDGSKGKVILETKSSMAAVEIGGGPWFG
 --SIIGKNGVSPGTRLSVAERLSQ-----LMMKNKDEKEVSDHSL-----

----DWGLTEENLSKKT-----VPF-----
 TWKGDTSNTPPELLKQALQVPLDLESALGLVPFFKPPGL
 ----EEKLAKEN-----

Figure 35